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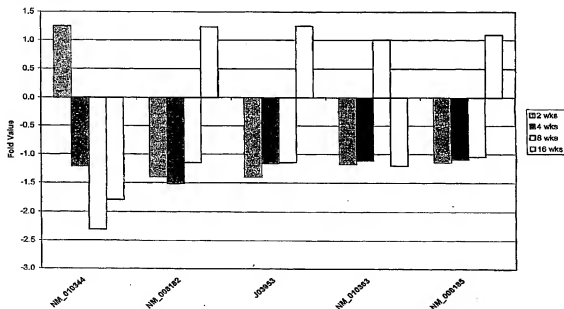
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[Continued on next page]

(54) Title: **DIAGNOSIS AND HYPERINSULINEMIA AND TYPE II DIABETES AND PROTECTION AGAINST SAME
BASED ON GENES DIFFERENTIALLY EXPRESSED IN PANCREAS CELLS (12.1)**



(57) Abstract: Mouse genes differentially expressed in comparisons of normal vs. hyperinsulinemic, hyperinsulinemic vs. type 2 diabetic, and normal vs. type 2 diabetes pancreas by gene chip analysis have been identified, as have corresponding human genes and proteins. The human molecules, or antagonists thereof, may be used for protection against hyperinsulinemia or type 2 diabetes, or their sequelae.



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**DIAGNOSIS OF HYPERINSULINEMIA AND TYPE II DIABETES AND
PROTECTION AGAINST SAME BASED ON GENES DIFFERENTIALLY
EXPRESSED IN PANCREAS CELLS (12.1)**

Cross-Reference to Related Applications

- 5 *Anti-Aging Applications.* Mice with a disrupted growth hormone receptor/binding protein gene enjoy an increased lifespan. In U.S. Prov. Appl. 60/485,222, filed July 8, 2003 (Kopchick8) mouse genes differentially expressed in comparisons of gene expression in growth hormone
10 receptor/binding protein gene-disrupted mouse livers and normal mouse livers were identified, as were corresponding human genes and proteins. It was suggested that the human molecules, or antagonists thereof, could be used for protection against faster-than-normal biological aging, or
15 to achieve slower-than-normal biological aging. It was also taught that the human molecules may also be used as markers of biological aging.

- In provisional application Ser. No. 60/474,606, filed June 2, 2003 (our docket Kopchick7-USA), our research group
20 used a gene chip to study the genetic changes in the liver of C57Bl/6J mice that occur at frequent intervals of the aging process. Differential hybridization techniques were used to identify mouse genes that are differentially expressed in mice, depending upon their age. The level of
25 gene expression of approximately 10,000 mouse genes (from the Amersham Codelink UniSet Mouse I Bioarray, product code: 300013) in the liver of mice with average ages of 35, 49, 56, 77, 118, 133, 207, 403, 558 and 725 days was determined. In essence, complementary RNA derived from mice
30 of different ages was screened for hybridization with oligonucleotide probes each specific to a particular mouse gene, each gene in turn representative of a particular mouse gene cluster (Unigene). Mouse genes which were differentially expressed (younger vs. older), as measured by
35 different levels of hybridization of the respective cRNA samples with the particular probe corresponding to that mouse gene, were identified. Related human genes and proteins were identified by sequence comparisons to the

mouse gene or protein. In the international appl. Kopchick7A-PCT, filed June 2, 2004, we added some additional studies of CIDE-A (see below).

5 In a like manner, the effect of aging on the expression of genes in mouse skeletal muscle was studied, see provisional application Ser. No. 60/566,068, filed April 29, 2004 (our docket Kopchick14-USA).

Anti-Diabetes Applications. In U.S. Provisional Appl. 10 Ser. No. 60/458,398 (our docket Kelder1-USA), filed March 31, 2003, members of our research group describe the identification of genes differentially expressed in normal vs. hyperinsulinemic, hyperinsulinemic vs. type II diabetic, or normal vs. type II diabetic mouse liver. Forward- and 15 reverse-substracted cDNA libraries were prepared, clones were isolated, and differentially expressed cDNA inserts were sequenced and compared with sequences in publicly available sequence databases. The corresponding mouse and human genes and proteins were identified.

20 The purpose of our research group's provisional application Ser. No. 60/460,415 (our docket: Kopchick6-USA), filed April 7, 2003, was similar, but complementary RNA, derived from RNA of mouse liver, was screened against a mouse gene chip. See also 60/506,716, filed Sept. 30, 2003 25 (Kopchick6.1).

Gene chip analyses have also been used to identify genes differentially expressed in normal vs. hyperinsulinemic, hyperinsulinemic vs. type II diabetic, or normal vs. type II diabetic mouse pancreas, see U.S. 30 Provisional Appl. 60/517,376, filed Nov. 6, 2003 (Kopchick12) and muscle, see U.S Provisional Appl. 60/547,512, filed Feb. 26, 2004 (Kopchick15).

Other differential hybridization applications. The use of differential hybridization to identify genes and proteins 35 is also described in our research group's Ser. No. PCT/US00/12145 (Kopchick 3A-PCT), Ser. No. PCT/US00/12366 (Kopchick4A-PCT), and Ser. No. 60/400,052 (Kopchick5).

All of the foregoing applications are hereby incorporated by reference in their entirety.

5 BACKGROUND OF THE INVENTION

Field of the Invention

The invention relates to various nucleic acid molecules and proteins, and their use in (1) diagnosing hyperinsulinemia and type II diabetes, or conditions
10 associated with their development, and (2) protecting mammals (including humans) against them.

Description of the Background Art

Anatomy and Physiology of the Pancreas

15 The pancreas is an elongated, tapered organ located across the back of the abdomen, behind the stomach. The right side of the organ (called the head) is the widest part of the organ and lies in the curve of the duodenum, the first division of the small intestine. The tapered left side
20 (called the body of the pancreas) extends slightly upward and ends near the spleen (called the tail). The pancreas is covered with a very thin connective tissue capsule which extends inward as septa, partitioning the gland into lobules.

25 The pancreas is composed of two major types of tissue. The bulk of the pancreas is composed of pancreatic exocrine cells and their associated ducts. The pancreatic exocrine cells are arranged in grape-like clusters called acini. The exocrine cells are packed with membrane-bound secretory
30 granules which contain digestive enzymes that are exocytosed into the lumen of the acinus. Exocrine secretions from acini flow successively through intercalated ducts, intralobular ducts, interlobular ducts and finally into the duodenum through the main pancreatic duct.

35 The enzymes secreted by the exocrine tissue in the pancreas help break down carbohydrates, fats, proteins, and acids in the duodenum. The three major classes are proteases, pancreatic lipases and amylase. These enzymes

travel down the pancreatic duct into the bile duct in an inactive form. When they enter the duodenum, they are activated. The exocrine tissue also secretes a bicarbonate to neutralize stomach acid in the duodenum. Secretion from the exocrine pancreas is regulated predominantly by three enzymes secreted by the enteric endocrine system: cholecystokinin, secretin, and gastrin.

Embedded within the exocrine tissue are roughly one million small clusters of cells called the Islets of Langerhans, which are the endocrine cells of the pancreas. The Islets of Langerhans are composed of four hormone-producing cell types: insulin-producing beta cells, glucagon-producing alpha cells, somatostatin-producing delta cells, and pancreatic polypeptide (PP)-producing cells. Beta cells make up ~70% of the cells in the islet and tend to be more centrally located. Alpha cells make up most of the rest of the islet and are generally near the periphery of the islet. Delta cells tend to be in the periphery of the islet, as are the least abundant PP-producing cells.

Insulin has the following functions: 1) It increases the rate of glucose metabolism, and glucose that is not needed immediately by the cells is changed into glycogen for storage (in the liver, skeletal muscles, and skin), and fat (especially for storage in the adipose tissue and liver); 2) It decreases the glucose level in the blood and increases glucose transport to skeletal, heart, smooth muscle, and fat cells. It does not affect glucose transport to the brain or red blood cells; 3) It increases transport of amino acids into the cells and causes an increase in protein synthesis; 4) It works along with growth hormone to promote growth.

With a lack of insulin, the liver will start breaking down glycogen and forming new glucose (gluconeogenesis). Fats will also be released into the blood in the form of free fatty acids. Amino acids will be released into the blood and very little protein synthesis will take place. Over time with a lack of insulin, acetone and ketone bodies will occur (due to largely burning fats instead of carbohydrates) - this can lead to a state of acidosis. Also "protein wasting" occurs and can lead to extreme weakness,

weight loss, and organ dysfunction.

Glucagon's main function is to break down glycogen into glucose and to simulate gluconeogenesis, thus increasing the blood glucose level. When blood glucose levels drop below 70 mg per 100 ml of blood, glucagon is secreted in large quantities to prevent hypoglycemia and make sure the brain is getting enough glucose (its major nutrient). If left uncontrolled, glucagon could deplete the liver of glycogen within four hours. Epinephrine and cortisol released by the adrenals also raise blood sugar, as does growth hormone released from the anterior pituitary.

Diseases affecting the Pancreas

Diabetes. A deficiency of insulin in the body results in diabetes mellitus, which affects about 13 million individuals in the United States. It is characterized by a high blood glucose (sugar) level and glucose spilling into the urine due to a deficiency of insulin. As more glucose concentrates in the urine, more water is excreted, resulting in extreme thirst, rapid weight loss, drowsiness, fatigue, and possibly dehydration. Because the cells of the diabetic cannot use glucose for fuel, the body uses stored protein and fat for energy, which leads to a buildup of acid (acidosis) in the blood. If this condition is prolonged, the person can fall into a diabetic coma, characterized by deep labored breathing and fruity-odored breath.

There are two types of diabetes mellitus, Type I and Type II. Type II diabetes is the predominant form found in the Western world; fewer than 8% of diabetic Americans have the type I disease.

Type I diabetes. In Type I diabetes, formerly called juvenile-onset or insulin-dependent diabetes mellitus, the pancreas cannot produce insulin. People with Type I diabetes must have daily insulin injections. But they need to avoid taking too much insulin because that can lead to insulin shock, which begins with a mild hunger. This is quickly followed by sweating, shallow breathing, dizziness, palpitations, trembling, and mental confusion. As the blood

sugar falls, the body tries to compensate by breaking down fat and protein to make more sugar. Eventually, low blood sugar leads to a decrease in the sugar supply to the brain, resulting in a loss of consciousness. Eating a sugary food can prevent insulin shock until appropriate medical measures can be taken.

Type I diabetics are often characterized by their low or absent levels of circulating endogenous insulin, i.e., hypoinsulinemia (1). Islet cell antibodies causing damage to the pancreas are frequently present at diagnosis. Injection of exogenous insulin is required to prevent ketosis and sustain life.

Type II diabetes. Type II diabetes, formerly called adult-onset or non-insulin-dependent diabetes mellitus (NIDDM), can occur at any age. The pancreas can produce insulin, but the cells do not respond to it.

Type II diabetes is a metabolic disorder that affects approximately 17 million Americans. It is estimated that another 10 million individuals are "prone" to becoming diabetic. These vulnerable individuals can become resistant to insulin, a pancreatic hormone that signals glucose (blood sugar) uptake by fat and muscle. In order to maintain normal glucose levels, the islet cells of the pancreas produce more insulin, resulting in a condition called hyperinsulinemia. When the pancreas can no longer produce enough insulin to compensate for the insulin resistance, and thereby maintain normal glucose levels, hyperglycemia (elevated blood glucose) results, and type II diabetes is diagnosed.

Early Type II diabetics are often characterized by hyperinsulinemia and resistance to insulin. Late Type II diabetics may be normoinsulinemic or hypoinsulinemic. Type II diabetics are usually not insulin dependent or prone to ketosis under normal circumstances.

Little is known about the disease progression from the normoinsulinemic state to the hyperinsulinemic state, and from the hyperinsulinemic state to the Type II diabetic state.

As stated above, type II diabetes is a metabolic disorder that is characterized by insulin resistance and impaired glucose-stimulated insulin secretion (2,3,4). However, Type II diabetes and atherosclerotic disease are viewed as consequences of having the insulin resistance syndrome (IRS) for many years (5). The current theory of the pathogenesis of Type II diabetes is often referred to as the "insulin resistance/islet cell exhaustion" theory. According to this theory, a condition causing insulin resistance compels the pancreatic islet cells to hypersecrete insulin in order to maintain glucose homeostasis. However, after many years of hypersecretion, the islet cells eventually fail and the symptoms of clinical diabetes are manifested. Therefore, this theory implies that, at some point, peripheral hyperinsulinemia will be an antecedent of Type II diabetes. Peripheral hyperinsulinemia can be viewed as the difference between what is produced by the β cell minus that which is taken up by the liver. Therefore, peripheral hyperinsulinemia can be caused by increased β cell production, decreased hepatic uptake or some combination of both. It is also important to note that it is not possible to determine the origin of insulin resistance once it is established since the onset of peripheral hyperinsulinemia leads to a condition of global insulin resistance.

Multiple environmental and genetic factors are involved in the development of insulin resistance, hyperinsulinemia and type II diabetes. An important risk factor for the development of insulin resistance, hyperinsulinemia and type II diabetes is obesity, particularly visceral obesity (6,7,8). Type II diabetes exists world-wide, but in developed societies, the prevalence has risen as the average age of the population increases and the average individual becomes more obese.

Obesity and Diabetes. Obesity is a serious and growing problem in the United States. Obesity-related health risks include high blood pressure, hardening of the arteries, cardiovascular disease, and Type II diabetes (also known as

non-insulin-dependent diabetes mellitus, Type II diabetes) (9,10,11). Recent studies show that 85% of the individuals with Type II diabetes are obese (12).

5 *Treatment of Diabetes.* For many years, treatment was insulin therapy for Type I and oral sulfonylureas and/or insulin therapy for Type II. Metformin (glucophage) was the first antidiabetic drug approved by FDA (May 1995) for the treatment of Type II diabetes since the oral sulfonylureas were introduced in 1984. Metformin promotes the use of insulin already in the blood. This May 1995 approval was followed by the September 1995 approval of another antidiabetic drug, Acarbose (precose). It slows down the digestion and absorption of complex sugars, which reduces blood sugar levels after meals.

10 Before 1982, insulin was purified from beef or pork pancreas. This was a problem for those diabetics allergic to animal insulin. Researchers produced a synthetic insulin called humulin. Approved by FDA in 1982, it was the first genetically engineered consumer health product manufactured for diabetics. Synthetic insulins can be produced in unlimited quantities.

20 Another possible treatment for diabetes includes surgically replacing the pancreas' endocrine tissues (islets of Langerhans) with healthy islet of Langerhans tissue grafts. Since 1988, 45 patients worldwide have undergone successful transplantation.

30 *Complications.* Complications of diabetes (end organ damage) include retinopathy, neuropathy, and nephropathy (traditionally designated as microvascular complications) as well as atherosclerosis (a macrovascular complication). Early stages of hyperglycemia can usually be controlled by an alteration in diet and increasing the amount of exercise, but drug treatment, including insulin, may be required. It has been shown that meticulous blood glucose control can often slow down or halt the progression of diabetic complications if caught early enough (1). However, tight metabolic control is extremely difficult to achieve.

Cystic Fibrosis

The major problem of cystic fibrosis, the number one genetic killer disease of children in the United States, is that the body overproduces thick, sticky mucus. The mucus blocks the pancreatic ducts, which impedes the flow of the pancreatic juices from the pancreas into the duodenum of the small intestines. Food cannot be properly digested. Without treatment, children with cystic fibrosis suffer from malnutrition and constant diarrhea; their average life expectancy is 21. Pancreatic enzyme preparations are usually used to minimize the disease's effects on the pancreas.

Pancreatic juices contain enzymes for digesting all three major food types (proteins, carbohydrates and fats), as well as quantities of bicarbonate ions, which play an important role in neutralizing the acid emptied by the stomach into the duodenum. The most important enzyme for fat digestion is pancreatic lipase, which is capable of changing fat into glycerol fatty acids and cholesterol. Hormones regulate pancreatic secretions. Food enters the small intestine. The hormones secretin and cholecystokinin cause the pancreas to create large quantities of fluid containing bicarbonate ions, which neutralizes the acid stomach contents.

Pancreatitis

Another common disease associated with the exocrine function of the pancreas is pancreatitis (inflammation of the pancreas), which can be either acute or chronic. The most common cause of acute pancreatitis is blockage by a gallstone of the main secretory duct from the pancreas as well as the common bile duct. When this happens, large quantities of pancreatic secretions pool in the pancreas and can digest the entire pancreas within a few hours. But because the islets of Langerhans are not adversely affected, the pancreas can continue secreting insulin. Acute pancreatitis is a condition demanding immediate medical attention. It is characterized by abdominal pain, vomiting, abdominal swelling and gas, fever, muscle aches, and a drop in blood pressure. When appropriately treated, the effects

of acute pancreatitis usually calm down within five to seven days. Treatment includes stopping oral consumption and providing nourishment only with intravenous fluids.

Chronic pancreatitis occurs when acute pancreatitis continues until pancreatic function is greatly diminished. Symptoms include persistent pain in the upper abdomen which can radiate to the back and last for days or weeks, with mild jaundice (yellow skin and eyes) and rapid weight loss. A person can have recurrent attacks over several years. This may result in secondary bacterial infections of the pancreas, calcium deficiencies, and Type II diabetes.

Pancreatic Cancer

Pancreatic cancer is the fourth leading cause of cancer deaths in the United States, affecting about 27,000 persons yearly. It is second only to colon cancer as a cause of death from gastrointestinal malignancy. It affects men twice as frequently as women and is more likely to develop after the age of 40. Pancreatic cancer risks increase with chronic pancreatitis, diabetes mellitus, genetic factors (more common in blacks than whites), smoking, excess alcohol consumption, high-fat diets, and exposure to industrial chemicals such as urea, naphthalene or benzidine. Symptoms include weight loss, abdominal pain, nausea, loss of appetite, itching, jaundice, and constipation. Abdominal stress may improve or worsen after eating, and the pain may increase after lying down. Because its symptoms mimic many other common health problems, it often goes undetected until it is too late to treat effectively.

When early diagnosis and early treatment are possible, however, survival chances increase. Imaging with endoscopic ultrasound may aid early diagnosis. Researchers are also rapidly building a library of potential genetic markers that indicate the onset of pancreatic cancer. Treatment includes chemotherapeutic drugs and traditional surgical techniques.

Animal Models

Transgenic Mouse Models of Diabetes or Diabetes Resistance. McGrane, et al., J. Biol. Chem. 263:11443-51

(1988) and Chen, et al., J. Biol. Chem., 269:15892-7 (1994) describe the genetic engineering of mice to express bovine growth hormone (bGH) or human growth hormone (hGH), respectively. These mice exhibited an enhanced growth phenotype. They also developed kidney lesions similar to those seen in diabetic glomerulosclerosis, see Yang, et al., Lab. Invest.; 68:62-70 (1993). Ogueta, et al., J. Endocrinol., 165: 321-8 (2000) reported that transgenic mice expressing bovine GH develop arthritic disorder and self-antibodies.

Growth hormone has many roles, ranging from regulation of protein, fat and carbohydrate metabolism to growth promotion. GH is produced in the somatotropic cells of the anterior pituitary and exerts its effects either through the GH-induced action of IGF-I, in the case of growth promotion, or by direct interaction with the GHR on target cells including liver, muscle, adipose, and kidney cells. Hyposecretion of GH during development leads to dwarfism, and hypersecretion before puberty leads to gigantism. In adults, hypersecretion of GH results in acromegaly, a clinical condition characterized by enlarged facial bones, hands, feet, fatigue and an increase in weight. Of those individuals with acromegaly, 25% develop type II diabetes. This may be due to insulin resistance caused by the high circulating levels of GH leading to high circulating levels of insulin (Kopchick et al., Annual Rev. Nutrition 1999. 19:437-61).

A further mode of GH action may be through the transcriptional regulation of a number of genes contributing to the physiological effects of GH.

Growth hormone genes and the proteins encoded by them can be converted into growth hormone antagonists by mutation, see Kopchick USP 5,350,836. Transgenic mice have been made that express the GH antagonists bGH-G119R or hGH G120R, and which exhibit a dwarf phenotype. Chen, et al., J. Biol. Chem., 263:15892-7 (1994); Chen, et al., Mol. Endocrinol., 5:1845-52 (1991); Chen, et al., Proc. Nat. Acad. Sci. USA 87:5061-5 (1990). These mice did not develop

kidney lesions. See Yang (1993), *supra*.

Chen, et al., *Endocrinol*, 136:660-7 (1995) compared the effect of streptozotocin treatment in normal nontransgenic mice, and in mice transgenic for (1) a GH receptor antagonist, the G119R mutant of bovine growth hormone or (2) the E117L-mutant of bGH. (According to Chen's ref. 24, these large GH transgenic streptozotocin-treated mice constitute an animal model for diabetes.) Glomerulosclerosis was seen in diabetic (STZ-treated) nontransgenic mice and in diabetic bGH-E117L mice, but not in diabetic bGH-G119R (GH antagonist) mice.

Two of the proteins which mediate growth hormone activity are the growth hormone receptor and the growth hormone binding protein, encoded by the same gene in mice (GHR/BP). It is possible to genetically engineer mice so that the gene encoding these proteins is disrupted ("knocked-out"; inactivated), see Zhou, et al., *Proc. Nat. Acad. Sci. (USA)*, 94:13215-20 (1997). Zhou, et al. inactivated the GHR/BP gene by replacing the 3' portion of exon 4 (which encodes a portion of the GH binding domains) and the 5' region of intron 4 with a neomycin gene cassette. The modified gene was introduced into the target mice by homologous recombination. Like mice expressing a GH antagonist, homozygous GHR/BP-KO mice exhibit a dwarf phenotype. GHR/BP-KO mice, made diabetic by streptozotocin treatment, are protected from the development of diabetes-associated nephropathy. Bellush, et al., *Endocrinol.*, 141:163-8 (2000).

High-Fat Diets. High-fat diets have been shown to induce both obesity and Type II diabetes in laboratory animals (13). Surwit and colleagues demonstrated that male C57BL/6J mice are extremely sensitive to the diabetogenic effects of a high-fat diet when initiated at weaning. At six months of age, high-fat fed animals had significantly elevated fasting blood-glucose and insulin levels and also demonstrated a decrease in insulin sensitivity (14). Ahren and colleagues (15) reported evidence of insulin resistance as well as diminished glucose-stimulated insulin release,

after feeding with a high-fat diet for 12 weeks. These mice also showed elevated levels of total cholesterol, triglycerides, and free fatty acids, another hallmark of Type II diabetes.

5

Identification of genes involved in hyperinsulinemia and type II diabetes, generally

Our attention recently has focused on the generation of pancreas mRNA expression profiles and the identification of genes involved in the genesis of the obesity-induced hyperinsulinemia and type-II diabetes. To date, no one has attempted to study the actual progression from the normal condition to that of hyperinsulinemia or from hyperinsulinemia to Type II diabetes in an attempt to identify genes that are up-regulated or down-regulated in the pancreas as the disease progresses.

In previous studies aimed at identifying genes involved in diabetes-induced glomerulosclerosis, differential display and traditional subtractive hybridization techniques were used (16-20). While effective for the identification of a few genes (e.g. hmunc13, PED/PEA-15, lactate dehydrogenase, amiloride sensitive sodium channel, ubiquitin-like protein, mdr 1, and a-amyloid protein precursor as well as a few novel genes), these techniques can be quite labor intensive. The PCR-based method of subtractive hybridization requires less starting material, and allows the simultaneous isolation of all differentially expressed cDNAs into two groups (up-regulated and down-regulated).

However, the PCR-based method of subtractive hybridization is also quite labor-intensive, produced large numbers of false positive candidates and ultimately resulted in the identification of a relatively limited number of differentially expressed genes. (see Kelder1-USA application).

In order to expand the number of genes that can be analyzed simultaneously, several groups have begun to utilize DNA microarray analysis to measure differences in gene expression between normal and diseased states.

However, these experiments have been limited in regards to the number of experimental conditions analyzed. DNA microarray analysis has been performed on normal, obese and diabetic mice (21). Also, the obesity and diabetes in the mouse models examined were caused by a specific endogenous genetic mutation (22). The differentially expressed genes in the above models may be very different from genes differentially expressed due to diet-induced obesity and Type-II diabetes.

The use of differential expression and related techniques to identify genes useful in the treatment of diabetes has been reviewed by Perfetti, et al., *Diabetes Technol. & Therapeut.*, 5(3): 421-3 (2003). Bernal-Mizrachi, et al., *Diabetes Metab. Res. Rev.* 19: 32-42 (2003).

Other papers of interest include:

Wada, et al., "Gene expression profile in streptozotocin-induced diabetic mice kidneys undergoing glomerulosclerosis", *Kidney Int.*, 59:1363-73 (2001);

Song, et al., "Cloning of a novel gene in the human kidney homologous to rat munc13S: its potential role in diabetic nephropathy", *Kidney Int.*, 53:1689-95 (1998);

Page, et al., "Isolation of diabetes-associated kidney genes using differential display", *Biochem. Biophys. Res. Comm.*, 232:49-53 (1997).

Peradi, "Subtractive hybridization claims: An efficient technique to detect overexpressed mRNAs in diabetic nephropathy," *Kidney Int.* 53:926-31 (1998).

Condorelli, *EMBO J.*, 17:3858-66 (1998).

Differential Expression in Pancreas

Lim, et al., *Biochem. Biophys. Res. Comm.*, 299: 806-12 (2002) studied gene expression in the pancreas of rats subjected to a 90% partial pancreatectomy (Px) (said to be a hyperglycemia-linked type II diabetes model). A total of 180 putative differentially expressed cDNAs were found. Tables list cDNAs over-expressed in normal rat pancreas (table 2)

or in the diabetes model (table 3). The highest expression ratio was 3.5 for the normal-favored genes and 3.0 for the Px-favored genes.

5 This was similar to an earlier study, Laybutt, et al., J. Biol. Chem., 277: 10912-10921 (2002).

See also Shalev, et al., "Oligonucleotide microarray analysis of intact human pancreatic islets: identification of glucose-responsive genes and a highly-regulated TGFbeta signaling pathway, Endocrinology, 143(9): 3695-8 (Sept. 10 2002); Mulder, et al., Differential changes in islet amyloid polypeptide (anylin) and insulin mRNA expression after high fat diet-induced insulin resistance in C57BL/6J mice," Metabolism, 49(12): 1518-22 (Dec. 2000).

15

Apoptosis and CIDE-A

Apoptosis is a form of programmed cell death that occurs in an active and controlled manner to eliminate unwanted cells. Apoptotic cells undergo an orchestrated 20 cascade of morphological changes such as membrane blebbing, nuclear shrinkage, chromatin condensation, and formation of apoptotic bodies which then undergo phagocytosis by neighboring cells. One of the hallmarks of cellular apoptosis is the cleavage of chromosomal DNA into discrete 25 oligonucleosomal size fragments. This orderly removal of unwanted cells minimizes the release of cellular components that may affect neighboring tissue. In contrast, membrane rupture and release of cellular components during necrosis often leads to tissue inflammation.

30 The process of apoptosis is highly conserved and involves the activation of the caspase cascade. Cohen, GM. (1997) Caspases: the executioners of apoptosis. Biochem. J. 326:1-16; Budihardjo, I., Oliver, H., Lutter, M., Luo, X., Wang, X. (1999) Biochemical pathways of caspase 35 activation during apoptosis. Annu. Rev. Cell. Dev. Biol. 15:269-290; Jacobson, M.D., Weil, M., Raff, M.C. (1997) Programmed cell death in animal development. Cell 88:347-354. Caspases are a family of serine proteases that are synthesized as inactive proenzymes. Their activation by

apoptotic signals such as CD95 (Fas) death receptor activation or tumor necrosis factor results in the cleavage of specific target proteins and execution of the apoptotic program. Apoptosis may occur by either an extrinsic pathway involving the activation of cell surface death receptors (DR) or by an intrinsic mitochondrial pathway. Yoon, J-H. Gores G.J. (2002) Death receptor-mediated apoptosis and the liver. *J. Hepatology* 37:400-410.

These pathways are not mutually exclusive and some cell types require the activation of both pathways for maximal apoptotic signaling. In type-I cells, death receptor activation leads to the recruitment and activation of caspases-8/10 and the rapid cleavage and activation of caspase-3 in a mitochondrial-independent manner.

Hepatocytes are members of the Type-II cells in which mitochondria are essential for DR-mediated apoptosis Scaffidi, C., Fulda, S., Srinivasan, A., Friesen, C., Li, F., Tomaselli, K.J., Debatin, K.M., Krammer, P.H., Peter, M.E. (1998) Two CD95 (APO-1/Fas) signaling pathways. *EMBO J.* 17:1675-1687. In this pathway, the pro-apoptotic protein Bid is truncated by activated caspases-8/10 and translocates to the mitochondria. Luo, X., Budihardjo, I., Zou, H., Slaughter, C., Wang, X. (1998) Bid, a Bcl2 interacting protein, mediates cytochrome c release from mitochondria in response to activation of cell surface death receptors. *Cell* 94:481-490; Li, H., Zhu, H., Xu, C.J., Yuan, J. (1998) Cleavage of BID by caspase 8 mediates the mitochondrial damage in the Fas pathway of apoptosis. *Cell* 94:491-501. This translocation leads to mitochondrial cytochrome c release and eventual activation of caspases-3 and 7 via cleavage by activated caspase-9.

One of the substrates for activated caspase-3 is the DNA fragmentation factor (DFF). DFF is composed of a 45 kDa regulatory subunit (DFF45) and a 40 kDa catalytic subunit (DFF40). Liu, X., Zou, H., Slaughter, C., Wang, X. (1997) DFF, a heterodimeric protein that functions downstream of caspase-3 to trigger DNA fragmentation during apoptosis. *Cell* 89:175-184. DFF45 cleavage by activated caspase-3 results in its dissociation from DFF40 and allows

the caspase-activated DNase (CAD) activity of DFF40 to cleave chromosomal DNA into oligonucleosomal size fragments. Liu, X., Li, P., Widlak, P., Zou, H., Luo, X., Garrard, W.T., Wang, X. (1998) The 40-kDa subunit of DNA

- 5 fragmentation factor induces DNA fragmentation and chromatin condensation during apoptosis. *Proc. Natl. Acad. Sci. USA.* 95:8461-8466; Halenbeck, R., MacDonald, H., Roulston, A., Chen, T.T., Conroy, L., Williams, L.T. (1998) CPAN, a human nuclease regulated by the caspase-sensitive inhibitor
- 10 DFF45. *Curr Biol.* 8:537-540; Nagata, S. (2000) Apoptotic DNA fragmentation. *Exp. Cell Res.* 256:12-8.

Recently, a novel family of cell-death-inducing DFF45-like effectors (CIDEs) have been identified that includes CIDE-A, CIDE-B and CIDE-3/FSP2. Inohara, N., Koseki, T.,

- 15 Chen, S., Wu, X., Nunez, G. (1998) CIDE, a novel family of cell death activators with homology to the 45 kDa subunit of the DNA fragmentation factor. *EMBO J.* 17:2526-2533;
- 20 Danesch, U., Hoeck, W., Ringold, G.M. (1992) Cloning and transcriptional regulation of a novel adipocyte-specific gene; FSP27. CAAT-enhancer-binding protein (C/EBP) and C/EBP-like proteins interact with sequences required for differentiation-dependent expression. *J. Biol. Chem.* 267:7185-7193; Liang, L., Zhao, M., Xu, Z., Yokoyama, K.K., Li, T. (2003) Molecular cloning and characterization of
- 25 CIDE-3, a novel member of the cell-death-inducing DNA-fragmentation-factor (DFF45)-like effector family. *Biochem. J.* 370:195-203.

The CIDEs contain an N-terminal domain that shares homology with the N-terminal region of DFF45 and may represent a

30 regulatory region via protein interaction. See Inohara, supra; Lugovskoy, A.A., Zhou, P., Chou, J.J., McCarty, J.S., Li, P., Wagner, G. (1999) Solution structure of the CIDE-N domain of CIDE-B and a model for CIDE-N/CIDE-N interactions in the DNA fragmentation pathway of apoptosis. *Cell* 9:747-

35 755. The family members also share a C-terminal domain that is necessary and sufficient for inducing cell death and DNA fragmentation; see Inohara supra. The overexpression of CIDE-A induces cell death that can be inhibited by DFF45. However, CIDE-A-induced apoptosis is not inhibited by

caspase-8 inhibitors thereby suggesting the presence of additional, caspase-independent, pathway(s) for the induction of apoptosis, see Inohara *supra*. Previous reports have indicated that human and mouse CIDE-A are expressed in several tissues such as brown adipose tissue (BAT) and heart and are localized to the mitochondria, Zhou, Z., Yon Toh, S., Chen, Z., Guo, K., Ng, C.P., Ponniah, S., Lin, S.C., Hong, W., Li, P. (2003) Cidea-deficient mice have lean phenotype and are resistant to obesity. *Nat. Genet.* 35:49-56. . In addition to the ability to induce apoptosis, CIDE-A can interact and inhibit UCP1 in BAT and may therefore play a role in regulating energy balance, see Zhou *supra*.

Previous reports have indicated that CIDE-A is not expressed in either adult human or mouse liver tissue, see Inohara *supra*, Zhou *supra*.

The human protein cell death activator CIDE-A is of particular interest because of its highly dramatic change in liver expression with age, first demonstrated in our Kopchick7 application, *supra*. CIDE-A expression is elevated in older normal mice. CIDE-A expression was studied for normal C57BI/6J mouse ages 35, 49, 77, 133, 207, 403 and 558 days. Expression is low at the first five data points, then rises sharply at 403 days, and again at 558 days. CIDE-A was therefore classified as an "unfavorable protein", i.e., it was taught that an antagonist to CIDE-A could retard biological aging.

In Kopchick7A-PCT we reported that CIDE-A is also prematurely expressed in hyperinsulinemic and type-II diabetic mouse liver tissue. CIDE-A expression also correlates with liver steatosis in diet-induced obesity, hyperinsulinemia and type-II diabetes. These observations suggest an additional pathway of apoptotic cell death in Non-Alcoholic Fatty Liver Disease (NAFLD) and that CIDE-A may play a role in this serious disease and potentially in liver dysfunction associated with type-II diabetes.

SUMMARY OF THE INVENTION

Differential hybridization techniques have been used to identify mouse genes that are differentially expressed in the pancreas of mice, depending upon their development of hyperinsulinemia or type II diabetes.

In essence, complementary RNA derived from normal mice, or mouse models of hyperinsulinemia or type II diabetes, was screened for hybridization with oligonucleotide probes each specific to a particular mouse database DNA, the latter being identified, by database accession number, by the gene manufacturer. Each database DNA in turn was also identified by the gene chip manufacturer as representative of a particular mouse gene cluster (Unigene).

In most cases, this database DNA sequence is a full length genomic DNA or cDNA sequence, and is therefore either identical to, or otherwise encodes the same protein as does, a natural full-length genomic DNA protein coding sequence. Those which don't present at least a partial sequence of a natural gene or its cDNA equivalent.

For the sake of simplicity, all of these mouse database DNA sequences, whether full-length or partial, and whether cDNA or genomic DNA, are referred to herein as "mouse genes". When only the genomic sequence is intended, we will refer specifically to "genomic DNA" or "gDNA".

The sequences in the protein databases are determined either by directly sequencing the protein or, more commonly, by sequencing a DNA, and then determining the translated amino acid sequence in accordance with the Genetic Code. All of the mouse sequences in the mouse polypeptide database are referred to herein as "mouse proteins" regardless of whether they are in fact full length sequences.

Mouse genes which were differentially expressed (normal vs. hyperinsulinemic, hyperinsulinemic vs. diabetic, or normal vs. diabetic), as measured by different levels of hybridization of the respective cRNA samples with the particular probe corresponding to that mouse gene) were identified.

Since the progression is from normal to

hyperinsulinemic, and thence from hyperinsulinemic to type II diabetic, one may define mammalian subjects as being more favored or less favored, with normal subjects being more favored than hyperinsulinemic subjects, and hyperinsulinemic subjects being more favored than type II diabetic subjects. The subjects' state may then be correlated with their gene expression activity.

The terms "normal" and "control" are used interchangeably in this specification, unless expressly stated otherwise. The control or normal subject is a mouse which is normal vis-a-vis fasting insulin and fasting glucose levels. The term "normal", as used herein, means normal relative to those parameters, and does not necessitate that the mouse be normal in every respect.

A mouse gene is said to have exhibited a favorable behavior if, for a particular mouse age of observation, its average level of expression in mice which are in a more favored state is **higher** than that in mice which are in a less favored state. A mouse gene is said to have exhibited an unfavorable behavior if, for a particular mouse age of observation, its average level of expression in mice which are in a more favored state is **lower** than that in mice which are in a less favored state.

When we observe the mice at several different ages, it is possible for their expression behavior to vary from time point to time point. For a given comparison of subjects, e.g., normal vs. hyperinsulinemic, we classify the mouse gene as favorable or unfavorable on the basis of the direction of the largest expression change, and it is the magnitude of this largest expression change, expressed as a ratio of greater to lesser, which is set forth in the Master Table 1 data for that mouse gene. Thus, if at 2 weeks, there was a 3-fold favorable behavior, and at 8 weeks, there was a 4-fold unfavorable behavior, and at all other time points, the behavior was weaker than 3-fold, the mouse gene would be classified as an unfavorable gene with respect to the subject comparison in question.

It will be appreciated that it may be that if the mouse gene were observed at an age other than one of the ages

noted in the Examples, we would have observed a still stronger differential expression behavior. Nonetheless, we must classify the mouse genes on the basis of the behavior which we actually observed, not the behavior which might have been observed at some other age.

We are particularly interested in mouse genes which exhibit strongly favorable or unfavorable differential expression behaviors. A behavior is considered strong if the ratio of the higher level to the lower level is at least two-fold.

However, a mouse gene may still be identified as favorable or unfavorable even if none of its observed behaviors are substantial as defined above. In general, we consider the consistency of its behaviors (that is, are all or most of the differential expression behaviors at different ages in the same direction, e.g., hyperinsulinemic higher than control), the magnitude of the behaviors (higher the better), and the expression behavior of structurally or functionally related mouse genes (a mouse gene is more likely to be identified as favorable on the basis of a weakly favorable behavior if it is related to other mouse genes which exhibited favorable, especially strongly favorable, behavior). If we considered a mouse gene with only weak differential expression behavior to be worthy of consideration on the basis of these criteria, then we listed it in Master Table 1 in the appropriate subtable.

Preferably, the differential behavior observed is both strong and consistent. Preferably, if related mouse genes were tested, they exhibit the same direction of differential expression behavior.

A mouse gene which was more strongly expressed in hyperinsulinemic tissue than in either normal or type II diabetic tissue (i.e., $C < HI$, $HI > D$) will be deemed both "unfavorable", by virtue of the control:hyperinsulinemic comparison, and "favorable", by virtue of the hyperinsulinemic:diabetic comparison. This is one of several possible "mixed" expression patterns.

Thus, we can subdivide the "favorables" into wholly and partially favorables. Likewise, we can subdivide the unfavorables into wholly and partially unfavorables. The genes/proteins with "mixed" expression patterns are, by definition, both partially favorable and partially unfavorable. In general, use of the wholly favorable or wholly unfavorable genes/proteins is preferred to use of the partially favorable or partially unfavorable ones.

It is evident from the foregoing that mixed genes/proteins are those exhibiting a combination of favorable and unfavorable behavior. A mixed gene/protein can be used as would a favorable gene/protein if its favorable behavior outweighs the unfavorable. It can be used as would an unfavorable gene/protein if its unfavorable behavior outweighs the favorable. Preferably, they are used in conjunction with other agents that affect their balance of favorable and unfavorable behavior. Use of mixed genes/proteins is, in general, less desirable than use of purely favorable or purely unfavorable genes/proteins, but it is not excluded.

It should be noted that a mouse gene is classified on the basis of the strongest C-HI behavior among the ages tested, the strongest HI-D behavior among the ages tested, and the strongest C-D behavior among the ages tested. If at least one of these three behaviors is significantly favorable, and none of the others of these three behaviors is significantly unfavorable, the mouse gene will be classified as wholly favorable and listed in subtable 1A of Master Table 1. However, that does not mean that it may not have exhibited a weaker but unfavorable expression behavior at some tested age.

The "favorable", "unfavorable" and "mixed" mouse proteins of the present invention include the mouse database proteins listed in the Master Table in the same row as a particular "favorable", "unfavorable" or "mixed" mouse gene, respectively. These proteins may be the exact translation product of the identified mouse gene (database DNA). However, if they were sequenced directly, they could be shorter or longer than that translation product. They could

also differ in sequence from the exact translation product as a result of post-translational modifications.

The mouse proteins of interest also include mouse proteins which, while not listed in the table, correspond to (i.e., homologous to, i.e., which could be aligned in a statistically significant manner to) such mouse proteins or genes, and mouse proteins which are at least substantially identical or conservatively identical to the listed mouse proteins.

Related human genes (database DNAs) and proteins were identified by searching a database comprising human DNAs or proteins for sequences corresponding to (i.e., homologous to, i.e., which could be aligned in a statistically significant manner to) the mouse gene or protein. More than one human protein may be identified as corresponding to a particular mouse chip probe and to a particular mouse gene.

Note that the terms "human genes" and "human proteins" are used in a manner analogous to that already discussed in the case of "mouse genes" and "mouse proteins".

As used herein, the term "corresponding" does not mean identical, but rather implies the existence of a statistically significant sequence similarity, such as one sufficient to qualify the human protein or gene as a homologous protein or DNA as defined below. The greater the degree of relationship as thus defined (i.e., by the statistical significance of each alignment used to connect the mouse cDNA to the human protein or gene, measured by an E value), the more close the correspondence. The connection may be direct (mouse gene to human protein) or indirect (e.g., mouse gene to human gene, human gene to human protein). By "mouse gene", we mean the mouse gene from which the gene chip DNA in question was derived.

In general, the human genes/proteins which most closely correspond, directly or indirectly, to the mouse genes are preferred, such as the one(s) with the highest, top two highest, top three highest, top four highest, top five highest, and top ten highest E values for the final

alignment in the connection process. The human genes/proteins deemed to correspond to our mouse genes are identified in the Master Tables.

5 Note that it is possible to identify homologous full-length human genes and proteins, if they are present in the database, even if the query mouse DNA or protein sequence is not a full-length sequence.

10 If there is no homologous full-length human gene or protein in the database, but there is a partial one, the latter may nonetheless be useful. For example, a partial protein may still have biological activity, and a molecule which binds the partial protein may also bind the full-length protein so as to antagonize a biological activity of the full-length protein. Likewise, a partial human gene may
15 encode a partial protein which has biological activity, or the gene may be useful in the design of a hybridization probe or in the design of a therapeutic antisense DNA.

The partial genes and protein sequences may of course also be used in the design of probes intended to identify
20 the full length gene or protein sequence.

For the sake of convenience, we refer to a human protein as favorable if (1) it is listed in Master Table 1 as corresponding to a favorable mouse gene, or (2) it is at
25 least substantially identical or conservatively identical to a listed protein per (1), or (3) it is a member of a human protein class listed in Master Table 2 (if provided) as corresponding to a favorable mouse gene. We define a human protein as unfavorable in an analogous manner. We may
30 further identify a human protein as being wholly favorable (see mouse genes of subtable 1A, wholly unfavorable (see mouse genes of subtable 1B), or mixed, i.e., both partially favorable and partially unfavorable (see mouse genes of subtable 1C).

35 Likewise, a human gene which encodes a particular human protein may be classified in the same way as the human protein which it encodes.

However, it should be noted that this classification is not based on the direct study of the expression of the human

gene/protein. of course, the human genes/proteins of ultimate interest will be the ones whose change in level of expression is, in fact, correlated, directly or inversely, with the change of state (normal, hyperinsulinemic, diabetic) of the subject.

After identifying related human genes and proteins, one may formulate agents useful in screening humans at risk for progression toward hyperinsulinemia or toward type II diabetes, or protecting humans at risk thereof from progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state.

Agents which bind the "favorable" and "unfavorable" nucleic acids (e.g., the agent is a substantially complementary nucleic acid hybridization probe), or the corresponding proteins (e.g., an antibody vs. the protein) may be used to evaluate whether a human subject is at increased or decreased risk for progression toward type II diabetes. A subject with one or more elevated "unfavorable" and/or one or more depressed "favorable" genes/proteins is at increased risk, and one with one or more elevated "favorable" and/or one or more depressed "unfavorable" genes/proteins is at decreased risk. One may further take into account whether the subject is normoinsulinemic or hyperinsulinemic at the time of the assay. If the subject is non-diabetic and normoinsulinemic, we are especially interested in the "favorable" and "unfavorable" genes/proteins corresponding to mouse genes differentially expressed in hyperinsulinemic vs. normal pancreas. If the subject is already hyperinsulinemic, yet non-diabetic, we are especially interested in the "favorable" and "unfavorable" genes/proteins corresponding to mouse genes differentially expressed in type II diabetic vs. hyperinsulinemic pancreas.

The assay may be used as a preliminary screening assay to select subjects for further analysis, or as a formal diagnostic assay.

The identification of the related genes and proteins may also be useful in protecting humans against these disorders.

Thus, Applicants contemplate:

5 (1) use of the "favorable" mouse DNAs (or fragments thereof) of the Master Tables (below) to isolate or identify related human DNAs;

(2) use of human DNAs, related to favorable mouse DNAs, to express the corresponding human proteins;

10 (3) use of the corresponding human proteins (and mouse proteins, if biologically active in humans), to protect against the disorder(s);

(4) use of the corresponding mouse or human proteins, or nucleic acid probes derived from the mouse or human genes, in diagnostic agents, in assays to measure progression toward hyperinsulinemia or type II diabetes, or protection against the disorder(s), or to estimate related end organ damage such as kidney damage; and

15 (5) use of the corresponding human or mouse genes therapeutically in gene therapy, to protect against the disorder(s).

Moreover Applicants contemplate:

(1) use of the "unfavorable" mouse DNAs (or fragments thereof) of the Master Tables to isolate or identify related human DNAs;

25 (2) use of the complement to the "unfavorable" mouse DNAs or related human DNAs, as antisense molecules to inhibit expression of the related human DNAs;

(3) use of the mouse or human DNAs to express the corresponding mouse or human proteins;

30 (4) use of the corresponding mouse or human proteins, in diagnostic agents, to measure progression toward hyperinsulinemia or type II diabetes, or protection against the disorder(s), or to estimate related end organ damage such as kidney damage;

35 (5) use of the corresponding mouse or human proteins in assays to determine whether a substance binds to (and hence may neutralize) the protein; and

(6) use of the neutralizing substance to protect

against the disorder(s).

Thus, DNAs of interest include those which specifically hybridize to the aforementioned mouse or human genes, and are thus of interest as hybridization assay reagents or for antisense therapy. They also include synthetic DNA sequences which encode the same polypeptide as is encoded by the database DNA, and thus are useful for producing the polypeptide in cell culture or in situ (i.e., gene therapy). Moreover, they include DNA sequences which encode polypeptides which are substantially structurally identical or conservatively identical in amino acid sequence to the mouse and human proteins identified in the Master Table 1, subtables 1A or 1C. Finally, they include DNA sequences which encode peptide (including antibody) antagonists of the proteins of Master Table 1, subtables 1B or 1C.

The related human DNAs may be identified by comparing the mouse sequence (or its AA translation product) to known human DNAs (and their AA translation products). Related human DNAs also may be identified by screening human cDNA or genomic DNA libraries using the mouse gene of the Master Table, or a fragment thereof, as a probe.

If the mouse gene of Master Table 1 is not full-length, and there is no closely corresponding full-length mouse gene in the sequence databank, then the mouse DNA may first be used as a hybridization probe to screen a mouse cDNA library to isolate the corresponding full-length sequence. Alternatively, the mouse DNA may be used as a probe to screen a mouse genomic DNA library.

Our animal models of hyperinsulinemia and diabetes are also obese. It is possible that the genes found to be favorable act indirectly by inhibiting obesity. Likewise, it is possible that the genes found to be unfavorable act indirectly by accentuating obesity. Consequently, it is within the compass of the present invention to use the favorable genes and proteins, or to use antagonists of the unfavorable genes and proteins, to protect against obesity,

as well as against sequelae of obesity such as hyperinsulinemia and diabetes.

Since type II diabetes is an age-related disease, the agents of the present invention may be used in conjunction with known anti-aging or anti-age-related disease agents. It is of particular interest to use the agents of the present invention in conjunction with an agent disclosed in one of the related applications cited above, in particular, an antagonist to CIDE-A, the latter having been taught in Kopchick7 and Kopchick7A-PCT.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Body weight gain (1(a)), fasting glucose (1(b)) and fasting insulin (1(c)) levels of mice on the HF or Std diets. Results reflect mean \pm SE of 50 mice on the high fat (HF) diet and 20 mice on the standard (Std) diet.

Figure 2. Pancreatic expression levels of glutathione peroxidase 1 (Gpx1, NM_008160) using RNA isolated from pancreas of individual diabetic HF mice and corresponding Std mice at different time points.

Figure 3. Pancreatic expression levels for additional glutathione peroxidase, S-transferase and synthetase genes exhibiting a consistent decrease in expression in the HF mice in comparison to Std mice at all four time points (top panel) or at three of the four time points (bottom panel).

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS OF THE INVENTION

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Full-Length vs. Partial Length Genes/Proteins

A "full length" gene is here defined as (1) a naturally occurring DNA sequence which begins with an initiation codon (almost always the Met codon, ATG), and ends with a stop codon in phase with said initiation codon (when introns, if any, are ignored), and thereby encodes a naturally occurring polypeptide with biological activity, or a naturally occurring precursor thereof, or (2) a synthetic DNA sequence which encodes the same polypeptide as that which is encoded by (1). The gene may, but need not, include introns.

A "full-length" protein is here defined as a naturally occurring protein encoded by a full-length gene, or a protein derived naturally by post-translational modification of such a protein. Thus, it includes mature proteins, proproteins, preproteins and preproproteins. It also includes substitution and extension mutants of such naturally occurring proteins.

Subjects

A mouse is considered to be a diabetic subject if, regardless of its fasting plasma insulin level, it has a fasting plasma glucose level of at least 190 mg/dL. A mouse is considered to be a hyperinsulinemic subject if its fasting plasma insulin level is at least 0.67 ng/mL and it does not qualify as a diabetic subject. A mouse is considered to be "normal" if it is neither diabetic nor hyperinsulinemic. Thus, normality is defined in a very limited manner.

A mouse is considered "obese" if its weight is at least 15% in excess of the mean weight for mice of its age and sex. A mouse which does not satisfy this standard may be characterized as "non-obese", the term "normal" being reserved for use in reference to glucose and insulin levels

as previously described.

A human is considered a diabetic subject if, regardless of his or her fasting plasma insulin level, the fasting plasma glucose level is at least 126 mg/dL. A human is considered a hyperinsulinemic subject if the fasting plasma insulin level is more than 26 micro International Units/mL (it is believed that this is equivalent to 1.08 ng/mL), and does not qualify as a diabetic subject. A human is considered to be "normal" if it is neither diabetic nor hyperinsulinemic. Thus, normality is defined in a very limited manner.

A human is considered "obese" if the body mass index (BMI) (weight divided by height²) is at least 30 kg/m². A human who does not satisfy this standard may be characterized as "non-obese", the term "normal" being reserved for use in reference to glucose and insulin levels as previously described.

A human is considered overweight if the BMI is at least 25 kg/m². Thus, we define overweight to include obese individuals, consistent with the recommendations of the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK). A human who does not satisfy this standard may be characterized as "non-overweight."

According to the Report of the Expert Committee on the Diagnosis and Classification of Diabetes Mellitus, Diabetes Care 20: 1183-97 (1997), the following are risk factors for diabetes type II:

older (e.g., at least 45; see below)

excessive weight (see below)

first-degree relative with diabetes mellitus

member of high risk ethnic group (black, Hispanic, Native American, Asian)

history of gestational diabetes mellitus or delivering a baby weighing more than 9 pounds (4.032 kg)

hypertensive ($>140/90$ mm Hg)

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HDL cholesterol level >35 mg/dL (0.90 mmol/L)

triglyceride level ≥ 250 mg/dL (2.83 mmol/L)

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Hence, in a preferred embodiment, the diagnostic and protective methods of the present invention are applied to human subjects exhibiting one or more of the aforementioned risk factors. Likewise, in a preferred embodiment, they are applied to human subjects who, while not diabetic, exhibit impaired glucose homeostasis (110 to <126 mg/dL).

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The risk of diabetes increases with age. Hence, in successive preferred embodiments, the age of the subjects is at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, and at least 75.

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With regard to excessive weight, NIDDK says that "The relative risk of diabetes increases by approximately 25 percent for each additional unit of BMI over 22." Hence, in successive preferred embodiments, the BMIs of the human subjects is at least 23, at least 24, at least 25 (i.e., overweight by our criterion), at least 26, at least 27, at least 28, at least 29, at least 30 (i.e., obese), at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, or over 40.

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Age-Related Diseases

Age-related (senescent) diseases include certain cancers, atherosclerosis, diabetes (type 2), osteoporosis, hypertension, depression, Alzheimer's, Parkinson's, glaucoma, certain immune system defects, kidney failure, and liver steatosis. In general, they are diseases for which the relative risk (comparing a subpopulation over age 55 to a

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suitably matched population under age 55) is at least 1.1.

Preferably, the agents of the present invention protect against one or more age-related diseases for at least a subpopulation of mature (post-puberty) adult subjects.

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Direct and Indirect Utility of Identified Nucleic Acid Sequences and Related Molecules

The mouse or human genes (or fragments thereof) may be used directly. For diagnostic or screening purposes, they (or specific binding fragments thereof) may be labeled and used as hybridization probes. For therapeutic purposes, they (or specific binding fragments thereof) may be used as antisense reagents to inhibit the expression of the corresponding gene, or of a sufficiently homologous gene of another species.

If the database DNA appears to be a full-length cDNA or gDNA, that is, it encodes an entire, functional, naturally occurring protein, then it may be used in the expression of that protein. Likewise, if the corresponding human gene is known in full-length, it may be used to express the human protein. Such expression may be in cell culture, with the protein subsequently isolated and administered exogenously to subjects who would benefit therefrom, or in vivo, i.e., administration by gene therapy. Naturally, any DNA encoding the same protein may be used for the same purpose, and a DNA encoding a protein which a fragment or a mutant of that naturally occurring protein which retains the desired activity, may be used for the purpose of producing the active fragment or mutant. The encoded protein of course has utility therapeutically and, in labeled or immobilized form, diagnostically.

The genes may also be used indirectly, that is, to identify other useful DNAs, proteins, or other molecules. We have attempted to determine whether the mouse genes disclosed herein have significant similarity to any known human DNA, and whether, in any of the six possible combinations of reference frame and strand, they encode a protein similar to a known human protein. If so, then it

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follows that the known human protein, and DNAs encoding that protein, may be used in a similar manner. In addition, if the known human protein is known to have additional homologues, then those homologous proteins, and DNAs encoding them, may be used in a similar manner.

There thus are several ways that a human protein homologue of interest can be identified by database searching, including but not limited to:

- 1) a DNA->DNA (BlastN) search for human database DNAs closely related to the mouse gene identifies a known human gene, and the sequence of the human protein is deduced by the Genetic Code;
- 2) a DNA->Protein (BlastX) search for human database proteins closely related to the translated DNA of the mouse gene identifies a known human protein; and
- 3) the sequence of the mouse protein is known, or is deduced by the Genetic Code, and a Protein->Protein (BlastP) search for closely related database proteins identifies a known human protein.

Once a known human gene is identified, it may be used in further BlastN or BlastX searches to identify other human genes or proteins. Once a known human protein is identified, it may be used in further BlastP searches to identify other human proteins.

Searches may also take cognizance, intermediately, of known genes and proteins other than mouse or human ones, e.g., use the mouse sequence to identify a known rat sequence and then the rat sequence to identify a human one.

If we have identified a mouse gene, and it encodes a mouse protein which appears similar to a human protein, then that human protein may be used (especially in humans) for

purposes analogous to the proposed use of the mouse protein in mice. Moreover, a specific binding fragment of an appropriate strand of the corresponding human gene (gDNA or cDNA) could be labeled and used as a hybridization probe (especially against samples of human mRNA or cDNA).

In determining whether the disclosed genes (gDNA or cDNA) have significant similarities to known DNAs (and their translated AA sequences to known proteins), one would generally use the disclosed gene as a query sequence in a search of a sequence database. The results of several such searches are set forth in the Examples. Such results are dependent, to some degree, on the search parameters. Preferred parameters are set forth in Example 1. The results are also dependent on the content of the database. While the raw similarity score of a particular target (database) sequence will not vary with content (as long as it remains in the database), its informational value (in bits), expected value, and relative ranking can change. Generally speaking, the changes are small.

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It will be appreciated that the nucleic acid and protein databases keep growing. Hence a later search may identify high scoring target sequences which were not uncovered by an earlier search because the target sequences were not previously part of a database.

Hence, in a preferred embodiment, the cognate DNAs and proteins include not only those set forth in the examples, but those which would have been highly ranked (top ten, more preferably top three, even more preferably top two, most preferably the top one) in a search run with the same parameters on the date of filing of this application.

If the known mouse or human database DNA appears to be a partial sequence (that is, partial relative to a cDNA or gDNA encoding the whole naturally occurring protein), it may be used as a hybridization probe to isolate the full-length DNA. If the partial DNA encodes a biologically functional fragment of the cognate protein, it may be used in a manner

similar to the full length DNA, i.e., to produce the functional fragment.

If we have indicated that an antagonist of a protein or other molecule is useful, then such an antagonist may be obtained by preparing a combinatorial library, as described below, of potential antagonists, and screening the library members for binding to the protein or other molecule in question. The binding members may then be further screened for the ability to antagonize the biological activity of the target. The antagonists may be used therapeutically, or, in suitably labeled or immobilized form, diagnostically.

If the identified mouse or human database DNA is related to a known protein, then substances known to interact with that protein (e.g., agonists, antagonists, substrates, receptors, second messengers, regulators, and so forth), and binding molecules which bind them, are also of utility. Such binding molecules can likewise be identified by screening a combinatorial library.

Isolation of Full Length DNAs Using Partial DNAs as probes

If it is determined that a DNA of the present invention is a partial DNA, and the cognate full length DNA is not listed in a sequence database, the available DNA may be used as a hybridization probe to isolate the full-length DNA from a suitable DNA library.

Stringent hybridization conditions are appropriate, that is, conditions in which the hybridization temperature is 5-10 deg. C. below the T_m of the DNA as a perfect duplex.

Identification and Isolation of Homologous Genes Using a DNA Probe

It may be that the sequence databases available do not include the sequence of any homologous gene (cDNA or gDNA), or at least of the homologous gene for a species of interest. However, given the cDNAs set forth above, one may readily obtain the homologous gene.

The possession of one DNA (the "starting DNA") greatly facilitates the isolation of homologous DNAs. If only a

partial DNA is known, this partial DNA may first be used as a probe to isolate the corresponding full length DNA for the same species, and that the latter may be used as the starting DNA in the search for homologous genes.

5 The starting DNA, or a fragment thereof, is used as a hybridization probe to screen a cDNA or genomic DNA library for clones containing inserts which encode either the entire homologous protein, or a recognizable fragment thereof. The minimum length of the hybridization probe is dictated by the
10 need for specificity. If the size of the library in bases is L , and the GC content is 50%, then the probe should have a length of at least l , where $L = 4^l$. This will yield, on average, a single perfect match in random DNA of L bases. The human cDNA library is about 10^6 bases and the human
15 genomic DNA library is about 10^{10} bases.

 The library is preferably derived from an organism which is known, on biochemical evidence, to produce a homologous protein, and more preferably from the genomic DNA or mRNA of cells of that organism which are likely to be
20 relatively high producers of that protein. A cDNA library (which is derived from an mRNA library) is especially preferred.

 If the organism in question is known to have substantially different codon preferences from that of the
25 organism whose relevant cDNA or genomic DNA is known, a synthetic hybridization probe may be used which encodes the same amino acid sequence but whose codon utilization is more similar to that of the DNA of the target organism. Alternatively, the synthetic probe may employ inosine as a
30 substitute for those bases which are most likely to be divergent, or the probe may be a mixed probe which mixes the codons for the source DNA with the preferred codons (encoding the same amino acid) for the target organism.

 By routine methods, the T_m of a perfect duplex of
35 starting DNA is determined. One may then select a hybridization temperature which is sufficiently lower than the perfect duplex T_m to allow hybridization of the starting DNA (or other probe) to a target DNA which is divergent from the starting DNA. A 1% sequence divergence typically lowers

the T_m of a duplex by 1-2°C, and the DNAs encoding homologous proteins of different species typically have sequence identities of around 50-80%. Preferably, the library is screened under conditions where the temperature is at least 20°C., more preferably at least 50°C., below the perfect duplex T_m . Since salt reduces the T_m , one ordinarily would carry out the search for DNAs encoding highly homologous proteins under relatively low salt hybridization conditions, e.g., <1M NaCl. The higher the salt concentration, and/or the lower the temperature, the greater the sequence divergence which is tolerated.

For the use of probes to identify homologous genes in other species, see, e.g., Schwinn, et al., J. Biol. Chem., 265:8183-89 (1990) (hamster 67-bp cDNA probe vs. human leukocyte genomic library; human 0.32kb DNA probe vs. bovine brain cDNA library, both with hybridization at 42°C in 6xSSC); Jenkins et al., J. Biol. Chem., 265:19624-31 (1990) (Chicken 770-bp cDNA probe vs. human genomic libraries; hybridization at 40°C in 50% formamide and 5xSSC); Murata et al., J. Exp. Med., 175:341-51 (1992) (1.2-kb mouse cDNA probe v. human eosinophil cDNA library; hybridization at 65°C in 6xSSC); Guyer et al., J. Biol. Chem., 265:17307-17 (1990) (2.95-kb human genomic DNA probe vs. porcine genomic DNA library; hybridization at 42°C in 5xSSC). The conditions set forth in these articles may each be considered suitable for the purpose of isolating homologous genes.

Corresponding (Homologous) Proteins and DNAs

In the case of a gene chip, the manufacturer of the gene chip determines which DNA to place at each position on the chip. This DNA may correspond in sequence to a genomic DNA, a cDNA, or a fragment of genomic or cDNA, and may be natural, synthetic or partially natural and partially synthetic in origin. The manufacturer of the gene chip will normally identify the DNA for a mouse gene chip as corresponding to a particular mouse gene, in which case it will be assumed that the alignments of chip DNA to mouse gene satisfies the homology criteria of the invention.

Usually, the gene chip manufacturer will provide a sequence database accession number for the mouse DNA. If so, to identify the corresponding mouse protein, we will first inspect the database record for that mouse DNA. Often, the mouse protein accession number will appear in that record or in a linked record. If it doesn't, the corresponding mouse protein can be identified by performing a BlastX search on a mouse protein database with the mouse database DNA sequence as the query sequence. Even if the protein sequence is not in the database, if the DNA sequence comprises a full-length coding sequence, the corresponding protein can be identified by translating the coding sequence in accordance with the Genetic Code.

A human protein can be said to be identifiable as corresponding (homologous) to a gene chip DNA if it is identified as corresponding (homologous) to the mouse gene (gDNA or cDNA, whole or partial) identified by the gene chip manufacturer as corresponding to that gene chip DNA.

In turn, it is identifiable as corresponding (homologous) to said identified mouse gene, if

(1) it can be aligned by BlastX directly to that mouse gene, and/or

(2) it is encoded by a human gene, or can be aligned to a human gene by BlastX, which in turn can be aligned by BlastN to said mouse gene and/or

(3) it can be aligned by BlastP to a mouse protein, the latter being encoded by said mouse gene, or aligned to said mouse gene BlastX,

where any alignment by BlastN, BlastP or BlastX is in accordance with the default parameters set forth below, and the expected value (E) of each alignment (the probability that such an alignment would have occurred by chance alone) is less than e^{-10} . (Note that because this is a negative

exponent, a value such as e^{-50} is less than e^{-10} .)

Desirably, two or all three of these conditions (1)-(3) are satisfied for the corresponding (homologous) human genes and
5 proteins.

A human gene is corresponding (homologous) to a mouse gene chip DNA, and hence to said identified mouse gene (or cDNA) and protein, if it encodes a corresponding
10 (homologous) human protein as defined above, or it can be aligned by BlastN to said mouse gene.

Preferably, for at least one of conditions (1)-(3), the E value is less than e^{-50} , more preferably less than e^{-60} , still more preferably less than e^{-70} , even more preferably
15 less than e^{-80} , considerably more preferably less than e^{-90} , and most preferably less than e^{-100} . Desirably, it is true for two or even all three of these conditions.

In constructing Master table 1, we generally used a BlastX (mouse gene vs. human protein) alignment E value
20 cutoff of e^{-50} . However, if there were no human proteins with that good an alignment to the mouse DNA in question, or if there were other reasons for including a particular human protein (e.g., a known functionality supportive of the
25 observed differential cognate mouse protein expression), then a human protein with a score worse (i.e., higher) than e^{-50} may appear in Master Table 1.

If the manufacturer of the gene chip identifies the gene chip DNA as corresponding to an EST, or other DNA which
30 is not a full-length mouse gene or cDNA, a longer (possibly full length) mouse gene or cDNA may be identified by a BlastN search of the mouse DNA database. Alternatively, the identified DNA may be used to conduct a BlastN search of a
35 human DNA database, or a BlastX search of a mouse or human protein database.

Thus, more generally, a human protein can be said to be identifiable as corresponding (homologous) to a gene chip DNA, or to a DNA identified by the manufacturer as

corresponding to that gene chip DNA, if

(1') it can be aligned directly to the gene chip or corresponding manufacturer identified DNA by BlastX. and/or

(2') it can be aligned to a human gene/cDNA by BlastX, whose genomic DNA (gDNA) or cDNA (DNA complementary to messenger RNA) in turn can be aligned to the gene chip or corresponding manufacturer identified DNA by BlastN, and/or

(3') it can be aligned to a mouse gene/cDNA by BlastX, whose gDNA or cDNA in turn can be aligned to the gene chip or corresponding manufacturer identified DNA by BlastN, and/or

(4') it can be aligned to a mouse protein by BlastP, which in turn can be aligned to the gene chip or corresponding manufacturer identified DNA by BlastX, and/or

(5') it can be aligned to a mouse protein by BlastP, which in turn can be aligned to a mouse gene/cDNA by BlastX, whose gDNA or cDNA can in turn be aligned to the gene chip or corresponding manufacturer identified DNA by BlastN;

where any alignment by BlastN, BlastP, or BlastX is in accordance with the default parameters set forth below, and the expected value (E) of each alignment (the probability that such an alignment would have occurred by chance alone) is less than e^{-10} . (Note that because this is a negative exponent, a value such as e^{-50} is less than e^{-10} .)

Preferably, two, three, four or all five of conditions (1')-(5') are satisfied.

Preferably, for at least one of conditions (1')-(5'), for at least the final alignment (i.e., vs. the human protein), the E value is less than e^{-50} , more preferably less than e^{-60} , , still more preferably less than e^{-70} , even more preferably less than e^{-80} , considerably more preferably less than e^{-90} , and most preferably less than e^{-100} .

Desirably, one or more of these standards of preference

are met for two, three, four or all five of conditions (1')-(5'). In particular, for those conditions in which the gene chip or corresponding manufacturer identified DNA is indirectly connected to the human protein by virtue of two or more successive alignments, the E value is preferably, so limited for all of said alignments in the connecting chain.

A human gene corresponds (is homologous) to a gene chip DNA or manufacturer identified corresponding DNA if it encodes a homologous human protein as defined above, or if it can be aligned either directly to that DNA, or indirectly through a mouse gene which can be aligned to said DNA, according to the conditions set forth above.

Master table 1 assembles a list of human protein corresponding to each of the mouse DNAs/proteins identified as related to the chip DNA. These human proteins form a set and can be given a percentile rank, with respect to E value, within that set. The human proteins of the present invention preferably are those scorers with a percentile rank of at least 50%, more preferably at least 60%, still more preferably at least 70%, even more preferably at least 80%, and most preferably at least 90%.

For each mouse gene (gDNA or cDNA) in Master Table 1, there is a particular human protein which provides the best alignment match as measured by BlastX, i.e., the human protein with the best score (lowest e-value). These human proteins form a subset of the set above and can be given a percentile rank within that subset, e.g., the human proteins with scores in the top 10% of that subset have a percentile rank of 90% or higher.

The human proteins of the present invention preferably are those best scorer subset proteins with a percentile rank within the subset of at least 50%, more preferably at least 60%, still more preferably at least 70%, even more preferably at least 80%, and most preferably at least 90%.

BlastN and BlastX report very low expected values as

"0.0". This does not truly mean that the expected value is exactly zero (since any alignment could occur by chance), but merely that it is so infinitesimal that it is not reported. The documentation does not state the cutoff value, but alignments with explicit E values as low as e^{-178} (624 bits) have been reported as nonzero values, while a score of 636 bits was reported as "0.0".

Functionally homologous human proteins are also of interest. A human protein may be said to be functionally homologous to the mouse gene if the human protein has at least one biological activity in common with the mouse protein encoded by said mouse gene.

The human proteins of interest also include those that are substantially and/or conservatively identical (as defined below) to the homologous and/or functionally homologous human proteins defined above.

Degree of Differential Expression

The degree of differential expression may be expressed as the ratio of the higher expression level to the lower expression level. Preferably, this is at least 2-fold, and more preferably, it is higher, such as at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, or at least 10-fold.

Most preferably, the human protein of interest corresponds to a mouse gene for which the degree of differential expression places it among the top 10% of the mouse genes in the appropriate subtable.

Relevance of Favorable and Unfavorable Genes

If a gene is down-regulated in more favored mammals, or up-regulated in less favored mammals, (i.e., an "unfavorable

gene") then several utilities are apparent.

First, the complementary strand of the gene, or a portion thereof, may be used in labeled form as a hybridization probe to detect messenger RNA and thereby monitor the level of expression of the gene in a subject. Elevated levels are indicative of progression, or propensity to progression, to a less favored state, and clinicians may take appropriate preventative, curative or ameliorative action.

Secondly, the messenger RNA product (or equivalent cDNA), the protein product, or a binding molecule specific for that product (e.g., an antibody which binds the product), or a downstream product which mediates the activity (e.g., a signaling intermediate) or a binding molecule (e.g., an antibody) therefor, may be used, preferably in labeled or immobilized form, as an assay reagent in an assay for said nucleic acid product, protein product, or downstream product (e.g., a signaling intermediate). Again, elevated levels are indicative of a present or future problem.

Thirdly, an agent which down-regulates expression of the gene may be used to reduce levels of the corresponding protein and thereby inhibit further damage. This agent could inhibit transcription of the gene in the subject, or translation of the corresponding messenger RNA. Possible inhibitors of transcription and translation include antisense molecules and repressor molecules. The agent could also inhibit a post-translational modification (e.g., glycosylation, phosphorylation, cleavage, GPI attachment) required for activity, or post-translationally modify the protein so as to inactivate it. Or it could be an agent which down- or up-regulated a positive or negative regulatory gene, respectively.

Fourthly, an agent which is an antagonist of the messenger RNA product or protein product of the gene, or of a downstream product through which its activity is manifested (e.g., a signaling intermediate), may be used to inhibit its activity.

This antagonist could be an antibody, a peptide, a

peptoid, a nucleic acid, a peptide nucleic acid (PNA) oligomer, a small organic molecule of a kind for which a combinatorial library exists (e.g., a benzodiazepine), etc. An antagonist is simply a binding molecule which, by
5 binding, reduces or abolishes the undesired activity of its target. The antagonist, if not an oligomeric molecule, is preferably less than 1000 daltons, more preferably less than 500 daltons.

Fifthly, an agent which degrades, or abets the
10 degradation of, that messenger RNA, its protein product or a downstream product which mediates its activity (e.g., a signaling intermediate), may be used to curb the effective period of activity of the protein.

If a gene is up-regulated in more favored mammals, or
15 down-regulated in less favored animals then the utilities are converse to those stated above.

First, the complementary strand of the gene, or a portion thereof, may be used in labeled form as a hybridization probe to detect messenger RNA and thereby
20 monitor the level of expression of the gene in a subject. Depressed levels are indicative of damage, or possibly of a propensity to damage, and clinicians may take appropriate preventative, curative or ameliorative action.

Secondly, the messenger RNA product, the equivalent
25 cDNA, protein product, or a binding molecule specific for those products, or a downstream product, or a signaling intermediate, or a binding molecule therefor, may be used, preferably in labeled or immobilized form, as an assay reagent in an assay for said protein product or downstream
30 product. Again, depressed levels are indicative of a present or future problem.

Thirdly, an agent which up-regulates expression of the gene may be used to increase levels of the corresponding protein and thereby inhibit further progression to a less
35 favored state. By way of example, it could be a vector which carries a copy of the gene, but which expresses the gene at higher levels than does the endogenous expression system. Or it could be an agent which up- or down-regulates a positive or negative regulatory gene.

Fourthly, an agent which is an agonist of the protein product of the gene, or of a downstream product through which its activity (of inhibition of progression to a less favored state) is manifested, or of a signaling intermediate
5 may be used to foster its activity.

Fifthly, an agent which inhibits the degradation of that protein product or of a downstream product or of a signaling intermediate may be used to increase the effective period of activity of the protein.
10

Mutant Proteins

The present invention also contemplates mutant proteins (peptides) which are substantially identical (as defined
15 below) to the parental protein (peptide). In general, the fewer the mutations, the more likely the mutant protein is to retain the activity of the parental protein. The effect of mutations is usually (but not always) additive. Certain individual mutations are more likely to be tolerated than
20 others.

A protein is more likely to tolerate a mutation which

- (a) is a substitution rather than an insertion or deletion;
- 25 (b) is an insertion or deletion at the terminus, rather than internally, or, if internal, is at a domain boundary, or a loop or turn, rather than in an alpha helix or beta strand;
- (c) affects a surface residue rather than an interior residue;
- 30 (d) affects a part of the molecule distal to the binding site;
- (e) is a substitution of one amino acid for another of similar size, charge, and/or hydrophobicity, and does not destroy a disulfide
35 bond or other crosslink; and
- (f) is at a site which is subject to substantial variation among a family of homologous proteins to which the protein of interest belongs.

These considerations can be used to design functional

mutants.

Surface vs. Interior Residues

5 Charged amino acid residues almost always lie on the surface of the protein. For uncharged residues, there is less certainty, but in general, hydrophilic residues are partitioned to the surface and hydrophobic residues to the interior. Of course, for a membrane protein, the membrane-spanning segments are likely to be rich in hydrophobic
10 residues.

Surface residues may be identified experimentally by various labeling techniques, or by 3-D structure mapping techniques like X-ray diffraction and NMR. A 3-D model of a homologous protein can be helpful.

15

Binding Site Residues

Residues forming the binding site may be identified by (1) comparing the effects of labeling the surface residues before and after complexing the protein to its target, (2)
20 labeling the binding site directly with affinity ligands, (3) fragmenting the protein and testing the fragments for binding activity, and (4) systematic mutagenesis (e.g., alanine-scanning mutagenesis) to determine which mutants destroy binding. If the binding site of a homologous
25 protein is known, the binding site may be postulated by analogy.

Protein libraries may be constructed and screened that a large family (e.g., 10^8) of related mutants may be evaluated simultaneously.

30 Hence, the mutations are preferably conservative modifications as defined below.

"Substantially Identical"

A mutant protein (peptide) is substantially identical
35 to a reference protein (peptide) if (a) it has at least 10% of a specific binding activity or a non-nutritional biological activity of the reference protein, and (b) is at least 50% identical in amino acid sequence to the reference protein (peptide). It is "substantially structurally

identical" if condition (b) applies, regardless of (a).

Percentage amino acid identity is determined by aligning the mutant and reference sequences according to a rigorous dynamic programming algorithm which globally aligns their sequences to maximize their similarity, the similarity being scored as the sum of scores for each aligned pair according to an unbiased PAM250 matrix, and a penalty for each internal gap of -12 for the first null of the gap and -4 for each additional null of the same gap. The percentage identity is the number of matches expressed as a percentage of the adjusted (i.e., counting inserted nulls) length of the reference sequence.

A mutant DNA sequence is substantially identical to a reference DNA sequence if they are structural sequences, and encoding mutant and reference proteins which are substantially identical as described above.

If instead they are regulatory sequences, they are substantially identical if the mutant sequence has at least 10% of the regulatory activity of the reference sequence, and is at least 50% identical in nucleotide sequence to the reference sequence. Percentage identity is determined as for proteins except that matches are scored +5, mismatches -4, the gap open penalty is -12, and the gap extension penalty (per additional null) is -4.

More preferably, the sequence is not merely substantially identical but rather is at least 51%, at least 66%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical in sequence to the reference sequence.

DNA sequences may also be considered "substantially identical" if they hybridize to each other under stringent conditions, i.e., conditions at which the T_m of the heteroduplex of the one strand of the mutant DNA and the more complementary strand of the reference DNA is not in excess of 10°C. less than the T_m of the reference DNA homoduplex. Typically this will correspond to a percentage identity of 85-90%.

"Conservative Modifications"

"Conservative modifications" are defined as

- (a) conservative substitutions of amino acids as hereafter defined; or
- 5 (b) single or multiple insertions (extension) or deletions (truncation) of amino acids at the termini.

Conservative modifications are preferred to other modifications. Conservative substitutions are preferred to
10 other conservative modifications.

"Semi-Conservative Modifications" are modifications which are not conservative, but which are (a) semi-conservative substitutions as hereafter defined; or (b)
15 single or multiple insertions or deletions internally, but at interdomain boundaries, in loops or in other segments of relatively high mobility. Semi-conservative modifications are preferred to nonconservative modifications. Semi-conservative substitutions are preferred to other semi-conservative modifications.

20 Non-conservative substitutions are preferred to other non-conservative modifications.

The term "conservative" is used here in an a priori sense, i.e., modifications which would be expected to preserve 3D structure and activity, based on analysis of the
25 naturally occurring families of homologous proteins and of past experience with the effects of deliberate mutagenesis, rather than post facto, a modification already known to conserve activity. Of course, a modification which is conservative a priori may, and usually is, also conservative
30 post facto.

Preferably, except at the termini, no more than about five amino acids are inserted or deleted at a particular locus, and the modifications are outside regions known to contain binding sites important to activity.

35 Preferably, insertions or deletions are limited to the termini.

A conservative substitution is a substitution of one amino acid for another of the same exchange group, the exchange groups being defined as follows

- I Gly, Pro, Ser, Ala (Cys) (and any nonbiogenic, neutral amino acid with a hydrophobicity not exceeding that of the aforementioned a.a.'s)
- 5 II Arg, Lys, His (and any nonbiogenic, positively-charged amino acids)
- III Asp, Glu, Asn, Gln (and any nonbiogenic negatively-charged amino acids)
- IV Leu, Ile, Met, Val (Cys) (and any nonbiogenic, aliphatic, neutral amino acid with a
- 10 hydrophobicity too high for I above)
- V Phe, Trp, Tyr (and any nonbiogenic, aromatic neutral amino acid with a hydrophobicity too high for I above).

Note that Cys belongs to both I and IV.

- 15 Residues Pro, Gly and Cys have special conformational roles. Cys participates in formation of disulfide bonds. Gly imparts flexibility to the chain. Pro imparts rigidity to the chain and disrupts α helices. These residues may be essential in certain regions of the polypeptide, but
- 20 substitutable elsewhere.

One, two or three conservative substitutions are more likely to be tolerated than a larger number.

- "Semi-conservative substitutions" are defined herein as being substitutions within supergroup I/II/III or within
- 25 supergroup IV/V, but not within a single one of groups I-V. They also include replacement of any other amino acid with alanine. If a substitution is not conservative, it preferably is semi-conservative.

- "Non-conservative substitutions" are substitutions
- 30 which are not "conservative" or "semi-conservative".

- "Highly conservative substitutions" are a subset of conservative substitutions, and are exchanges of amino acids within the groups Phe/Tyr/Trp, Met/Leu/Ile/Val, His/Arg/Lys, Asp/Glu and Ser/Thr/Ala. They are more likely to be
- 35 tolerated than other conservative substitutions. Again, the smaller the number of substitutions, the more likely they are to be tolerated.

"Conservatively Identical"

A protein (peptide) is conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by conservative modifications, the protein (peptide) remaining at least seven amino acids long if the reference protein (peptide) was at least seven amino acids long.

A protein is at least semi-conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by semi-conservative or conservative modifications.

A protein (peptide) is nearly conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by one or more conservative modifications and/or a single nonconservative substitution.

It is highly conservatively identical if it differs, if at all, solely by highly conservative substitutions. Highly conservatively identical proteins are preferred to those merely conservatively identical. An absolutely identical protein is even more preferred.

The core sequence of a reference protein (peptide) is the largest single fragment which retains at least 10% of a particular specific binding activity, if one is specified, or otherwise of at least one specific binding activity of the referent. If the referent has more than one specific binding activity, it may have more than one core sequence, and these may overlap or not.

If it is taught that a peptide of the present invention may have a particular similarity relationship (e.g., markedly identical) to a reference protein (peptide), preferred peptides are those which comprise a sequence having that relationship to a core sequence of the reference protein (peptide), but with internal insertions or deletions in either sequence excluded. Even more preferred peptides are those whose entire sequence has that relationship, with the same exclusion, to a core sequence of that reference protein (peptide).

Library

The term "library" generally refers to a collection of chemical or biological entities which are related in origin, structure, and/or function, and which can be screened simultaneously for a property of interest.

Libraries may be classified by how they are constructed (natural vs. artificial diversity; combinatorial vs. noncombinatorial), how they are screened (hybridization, expression, display), or by the nature of the screened library members (peptides, nucleic acids, etc.).

In a "natural diversity" library, essentially all of the diversity arose without human intervention. This would be true, for example, of messenger RNA extracted from a non-engineered cell.

In a "synthetic diversity" library, essentially all of the diversity arose deliberately as a result of human intervention. This would be true for example of a combinatorial library; note that a small level of natural diversity could still arise as a result of spontaneous mutation. It would also be true of a noncombinatorial library of compounds collected from diverse sources, even if they were all natural products.

In a "non-natural diversity" library, at least some of the diversity arose deliberately through human intervention.

In a "controlled origin" library, the source of the diversity is limited in some way. A limitation might be to cells of a particular individual, to a particular species, or to a particular genus, or, more complexly, to individuals of a particular species who are of a particular age, sex, physical condition, geographical location, occupation and/or familial relationship. Alternatively or additionally, it might be to cells of a particular tissue or organ. Or it could be cells exposed to particular pharmacological, environmental, or pathogenic conditions. Or the library could be of chemicals, or a particular class of chemicals, produced by such cells.

In a "controlled structure" library, the library members are deliberately limited by the production conditions to particular chemical structures. For example,

if they are oligomers, they may be limited in length and monomer composition, e.g. hexapeptides composed of the twenty genetically encoded amino acids.

5 Hybridization Library

 In a hybridization library, the library members are nucleic acids, and are screened using a nucleic acid hybridization probe. Bound nucleic acids may then be amplified, cloned, and/or sequenced.

10

Expression Library

 In an expression library, the screened library members are gene expression products, but one may also speak of an underlying library of genes encoding those products. The library is made by subcloning DNA encoding the library members (or portions thereof) into expression vectors (or into cloning vectors which subsequently are used to construct expression vectors), each vector comprising an expressible gene encoding a particular library member, introducing the expression vectors into suitable cells, and expressing the genes so the expression products are produced.

 In one embodiment, the expression products are secreted, so the library can be screened using an affinity reagent, such as an antibody or receptor. The bound expression products may be sequenced directly, or their sequences inferred by, e.g., sequencing at least the variable portion of the encoding DNA.

 In a second embodiment, the cells are lysed, thereby exposing the expression products, and the latter are screened with the affinity reagent.

 In a third embodiment, the cells express the library members in such a manner that they are displayed on the surface of the cells, or on the surface of viral particles produced by the cells. (See display libraries, below).

 In a fourth embodiment, the screening is not for the ability of the expression product to bind to an affinity reagent, but rather for its ability to alter the phenotype of the host cell in a particular detectable manner. Here,

the screened library members are transformed cells, but there is a first underlying library of expression products which mediate the behavior of the cells, and a second underlying library of genes which encode those products.

5

Display Library

In a display library, the library members are each conjugated to, and displayed upon, a support of some kind. The support may be living (a cell or virus), or nonliving (e.g., a bead or plate).

10

If the support is a cell or virus, display will normally be effectuated by expressing a fusion protein which comprises the library member, a carrier moiety allowing integration of the fusion protein into the surface of the cell or virus, and optionally a lining moiety. In a variation on this theme, the cell coexpresses a first fusion comprising the library member and a linking moiety L1, and a second fusion comprising a linking moiety L2 and the carrier moiety. L1 and L2 interact to associate the first fusion with the second fusion and hence, indirectly, the library member with the surface of the cell or virus.

15

20

Soluble Library

In a soluble library, the library members are free in solution. A soluble library may be produced directly, or one may first make a display library and then release the library members from their supports.

25

Encapsulated Library

In an encapsulated library, the library members are inside cells or liposomes. Generally speaking, encapsulated libraries are used to store the library members for future use; the members are extracted in some way for screening purposes. However, if they differentially affect the phenotype of the cells, they may be screened indirectly by screening the cells.

30

35

cDNA Library

A cDNA library is usually prepared by extracting RNA

from cells of particular origin, fractionating the RNA to isolate the messenger RNA (mRNA has a poly(A) tail, so this is usually done by oligo-dT affinity chromatography), synthesizing complementary DNA (cDNA) using reverse transcriptase, DNA polymerase, and other enzymes, subcloning the cDNA into vectors, and introducing the vectors into cells. Often, only mRNAs or cDNAs of particular sizes will be used, to make it more likely that the cDNA encodes a functional polypeptide.

10 A cDNA library explores the natural diversity of the transcribed DNAs of cells from a particular source. It is not a combinatorial library.

A cDNA library may be used to make a hybridization library, or it may be used as an (or to make) expression library.

Genomic DNA Library

A genomic DNA library is made by extracting DNA from a particular source, fragmenting the DNA, isolating fragments of a particular size range, subcloning the DNA fragments into vectors, and introducing the vectors into cells.

Like a cDNA library, a genomic DNA library is a natural diversity library, and not a combinatorial library. A genomic DNA library may be used the same way as a cDNA library.

Synthetic DNA library

A synthetic DNA library may be screened directly (as a hybridization library), or used in the creation of an expression or display library of peptides/proteins.

Combinatorial Libraries

The term "combinatorial library" refers to a library in which the individual members are either systematic or random combinations of a limited set of basic elements, the properties of each member being dependent on the choice and location of the elements incorporated into it. Typically, the members of the library are at least capable of being screened simultaneously. Randomization may be complete or

partial; some positions may be randomized and others predetermined, and at random positions, the choices may be limited in a predetermined manner. The members of a combinatorial library may be oligomers or polymers of some kind, in which the variation occurs through the choice of monomeric building block at one or more positions of the oligomer or polymer, and possibly in terms of the connecting linkage, or the length of the oligomer or polymer, too. Or the members may be nonoligomeric molecules with a standard core structure, like the 1,4-benzodiazepine structure, with the variation being introduced by the choice of substituents at particular variable sites on the core structure. Or the members may be nonoligomeric molecules assembled like a jigsaw puzzle, but wherein each piece has both one or more variable moieties (contributing to library diversity) and one or more constant moieties (providing the functionalities for coupling the piece in question to other pieces).

Thus, in a typical combinatorial library, chemical building blocks are at least partially randomly combined into a large number (as high as 10^{15}) of different compounds, which are then simultaneously screened for binding (or other) activity against one or more targets.

In a "simple combinatorial library", all of the members belong to the same class of compounds (e.g., peptides) and can be synthesized simultaneously. A "composite combinatorial library" is a mixture of two or more simple libraries, e.g., DNAs and peptides, or peptides, peptoids, and PNAs, or benzodiazepines and carbamates. The number of component simple libraries in a composite library will, of course, normally be smaller than the average number of members in each simple library, as otherwise the advantage of a library over individual synthesis is small.

Libraries of thousands, even millions, of random oligopeptides have been prepared by chemical synthesis (Houghten et al., *Nature*, 354:84-6(1991)), or gene expression (Marks et al., *J Mol Biol*, 222:581-97(1991)), displayed on chromatographic supports (Lam et al., *Nature*, 354:82-4(1991)), inside bacterial cells (Colas et al., *Nature*, 380:548-550(1996)), on bacterial pili (Lu,

Bio/Technology, 13:366-372(1990)), or phage (Smith, Science, 228:1315-7(1985)), and screened for binding to a variety of targets including antibodies (Valadon et al., J Mol Biol, 261:11-22(1996)), cellular proteins (Schmitz et al., J Mol Biol, 260:664-677(1996)), viral proteins (Hong and Boulanger, Embo J, 14:4714-4727(1995)), bacterial proteins (Jacobsson and Frykberg, Biotechniques, 18:878-885(1995)), nucleic acids (Cheng et al., Gene, 171:1-8(1996)), and plastic (Siani et al., J Chem Inf Comput Sci, 34:588-593(1994)).

Libraries of proteins (Ladner, USP 4,664,989), peptoids (Simon et al., Proc Natl Acad Sci U S A, 89:9367-71(1992)), nucleic acids (Ellington and Szostak, Nature, 246:818(1990)), carbohydrates, and small organic molecules (Eichler et al., Med Res Rev, 15:481-96(1995)) have also been prepared or suggested for drug screening purposes.

The first combinatorial libraries were composed of peptides or proteins, in which all or selected amino acid positions were randomized. Peptides and proteins can exhibit high and specific binding activity, and can act as catalysts. In consequence, they are of great importance in biological systems.

Nucleic acids have also been used in combinatorial libraries. Their great advantage is the ease with which a nucleic acid with appropriate binding activity can be amplified. As a result, combinatorial libraries composed of nucleic acids can be of low redundancy and hence, of high diversity.

There has also been much interest in combinatorial libraries based on small molecules, which are more suited to pharmaceutical use, especially those which, like benzodiazepines, belong to a chemical class which has already yielded useful pharmacological agents. The techniques of combinatorial chemistry have been recognized as the most efficient means for finding small molecules that act on these targets. At present, small molecule combinatorial chemistry involves the synthesis of either pooled or discrete molecules that present varying arrays of functionality on a common scaffold. These compounds are

grouped in libraries that are then screened against the target of interest either for binding or for inhibition of biological activity.

The size of a library is the number of molecules in it.

- 5 The simple diversity of a library is the number of unique structures in it. There is no formal minimum or maximum diversity. If the library has a very low diversity, the library has little advantage over just synthesizing and screening the members individually. If the library is of
10 very high diversity, it may be inconvenient to handle, at least without automatizing the process. The simple diversity of a library is preferably at least 10, 10E2, 10E3, 10E4, 10E6, 10E7, 10E8 or 10E9, the higher the better under most circumstances. The simple diversity is usually
15 not more than 10E15, and more usually not more than 10E10.

- The average sampling level is the size divided by the simple diversity. The expected average sampling level must be high enough to provide a reasonable assurance that, if a given structure were expected, as a consequence of the
20 library design, to be present, that the actual average sampling level will be high enough so that the structure, if satisfying the screening criteria, will yield a positive result when the library is screened. Thus, the preferred average sampling level is a function of the detection limit,
25 which in turn is a function of the strength of the signal to be screened.

- There are more complex measures of diversity than simple diversity. These attempt to take into account the degree of structural difference between the various unique
30 sequences. These more complex measures are usually used in the context of small organic compound libraries, see below.

- The library members may be presented as solutes in solution, or immobilized on some form of support. In the latter case, the support may be living (cell, virus) or
35 nonliving (bead, plate, etc.). The supports may be separable (cells, virus particles, beads) so that binding and nonbinding members can be separated, or nonseparable (plate). In the latter case, the members will normally be placed on addressable positions on the support. The

advantage of a soluble library is that there is no carrier moiety that could interfere with the binding of the members to the support. The advantage of an immobilized library is that it is easier to identify the structure of the members which were positive.

When screening a soluble library, or one with a separable support, the target is usually immobilized. When screening a library on a nonseparable support, the target will usually be labeled.

Oligonucleotide Libraries

An oligonucleotide library is a combinatorial library, at least some of whose members are single-stranded oligonucleotides having three or more nucleotides connected by phosphodiester or analogous bonds. The oligonucleotides may be linear, cyclic or branched, and may include non-nucleic acid moieties. The nucleotides are not limited to the nucleotides normally found in DNA or RNA. For examples of nucleotides modified to increase nuclease resistance and chemical stability of aptamers, see Chart 1 in Osborne and Ellington, Chem. Rev., 97: 349-70 (1997). For screening of RNA, see Ellington and Szostak, Nature, 346: 818-22 (1990).

There is no formal minimum or maximum size for these oligonucleotides. However, the number of conformations which an oligonucleotide can assume increases exponentially with its length in bases. Hence, a longer oligonucleotide is more likely to be able to fold to adapt itself to a protein surface. On the other hand, while very long molecules can be synthesized and screened, unless they provide a much superior affinity to that of shorter molecules, they are not likely to be found in the selected population, for the reasons explained by Osborne and Ellington (1997). Hence, the libraries of the present invention are preferably composed of oligonucleotides having a length of 3 to 100 bases, more preferably 15 to 35 bases. The oligonucleotides in a given library may be of the same or of different lengths.

Oligonucleotide libraries have the advantage that libraries of very high diversity (e.g., 10^{15}) are feasible,

and binding molecules are readily amplified in vitro by polymerase chain reaction (PCR). Moreover, nucleic acid molecules can have very high specificity and affinity to targets.

5 In a preferred embodiment, this invention prepares and screens oligonucleotide libraries by the SELEX method, as described in King and Famulok, *Molec. Biol. Repts.*, 20: 97-107 (1994); L. Gold, C. Tuerk. *Methods of producing nucleic acid ligands*, US#5595877; Oliphant et al. *Gene* 44:177
10 (1986).

The term "aptamer" is conferred on those oligonucleotides which bind the target protein. Such aptamers may be used to characterize the target protein, both directly (through identification of the aptamer and the
15 points of contact between the aptamer and the protein) and indirectly (by use of the aptamer as a ligand to modify the chemical reactivity of the protein).

In a classic oligonucleotide, each nucleotide (monomeric unit) is composed of a phosphate group, a sugar moiety, and
20 either a purine or a pyrimidine base. In DNA, the sugar is deoxyribose and in RNA it is ribose. The nucleotides are linked by 5'-3' phosphodiester bonds.

The deoxyribose phosphate backbone of DNA can be modified to increase resistance to nuclease and to increase
25 penetration of cell membranes. Derivatives such as mono- or dithiophosphates, methyl phosphonates, boranophosphates, formacetals, carbamates, siloxanes, and dimethylenethio-sulfoxideo- and-sulfo- linked species are known in the art.

30 Peptide Library

A peptide is composed of a plurality of amino acid residues joined together by peptidyl (-NHCO-) bonds. A biogenic peptide is a peptide in which the residues are all
35 genetically encoded amino acid residues; it is not necessary that the biogenic peptide actually be produced by gene expression.

Amino acids are the basic building blocks with which peptides and proteins are constructed. Amino acids possess

both an amino group ($-\text{NH}_2$) and a carboxylic acid group ($-\text{COOH}$). Many amino acids, but not all, have the alpha amino acid structure $\text{NH}_2\text{-CHR-COOH}$, where R is hydrogen, or any of a variety of functional groups.

5 Twenty amino acids are genetically encoded: Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Proline, Serine, Threonine, Tryptophan, Tyrosine, and Valine. Of these, all
10 save Glycine are optically isomeric, however, only the L-form is found in humans. Nevertheless, the D-forms of these amino acids do have biological significance; D-Phe, for example, is a known analgesic.

Many other amino acids are also known, including: 2-
15 Amino adipic acid; 3-Amino adipic acid; beta-Aminopropionic acid; 2-Aminobutyric acid; 4-Aminobutyric acid (Piperidinic acid); 6-Aminocaproic acid; 2-Aminoheptanoic acid; 2-Aminoisobutyric acid; 3-Aminoisobutyric acid; 2-Aminopimelic acid; 2,4-Diaminobutyric acid; Desmosine; 2,2'-
20 Diaminopimelic acid; 2,3-Diaminopropionic acid; N-Ethylglycine; N-Ethylasparagine; Hydroxylysine; allo-Hydroxylysine; 3-Hydroxyproline; 4-Hydroxyproline; Isodesmosine; allo-Isoleucine; N-Methylglycine (Sarcosine); N-Methylisoleucine; N-Methylvaline; Norvaline; Norleucine;
25 and Ornithine.

Peptides are constructed by condensation of amino acids and/or smaller peptides. The amino group of one amino acid (or peptide) reacts with the carboxylic acid group of a second amino acid (or peptide) to form a peptide ($-\text{NHCO}-$)
30 bond, releasing one molecule of water. Therefore, when an amino acid is incorporated into a peptide, it should, technically speaking, be referred to as an amino acid residue. The core of that residue is the moiety which excludes the $-\text{NH}$ and $-\text{CO}$ linking functionalities which
35 connect it to other residues. This moiety consists of one or more main chain atoms (see below) and the attached side chains.

The main chain moiety of each amino acid consists of the $-\text{NH}$ and $-\text{CO}$ linking functionalities and a core main

chain moiety. Usually the latter is a single carbon atom. However, the core main chain moiety may include additional carbon atoms, and may also include nitrogen, oxygen or sulfur atoms, which together form a single chain. In a preferred embodiment, the core main chain atoms consist solely of carbon atoms.

The side chains are attached to the core main chain atoms. For alpha amino acids, in which the side chain is attached to the alpha carbon, the C-1, C-2 and N-2 of each residue form the repeating unit of the main chain, and the word "side chain" refers to the C-3 and higher numbered carbon atoms and their substituents. It also includes H atoms attached to the main chain atoms.

Amino acids may be classified according to the number of carbon atoms which appear in the main chain between the carbonyl carbon and amino nitrogen atoms which participate in the peptide bonds. Among the 150 or so amino acids which occur in nature, alpha, beta, gamma and delta amino acids are known. These have 1-4 intermediary carbons. Only alpha amino acids occur in proteins. Proline is a special case of an alpha amino acid; its side chain also binds to the peptide bond nitrogen.

For beta and higher order amino acids, there is a choice as to which main chain core carbon a side chain other than H is attached to. The preferred attachment site is the C-2 (alpha) carbon, i.e., the one adjacent to the carboxyl carbon of the -CO linking functionality. It is also possible for more than one main chain atom to carry a side chain other than H. However, in a preferred embodiment, only one main chain core atom carries a side chain other than H.

A main chain carbon atom may carry either one or two side chains; one is more common. A side chain may be attached to a main chain carbon atom by a single or a double bond; the former is more common.

A simple combinatorial peptide library is one whose members are peptides having three or more amino acids connected via peptide bonds.

The peptides may be linear, branched, or cyclic, and may covalently or noncovalently include nonpeptidyl

moieties. The amino acids are not limited to the naturally occurring or to the genetically encoded amino acids.

A biased peptide library is one in which one or more (but not all) residues of the peptides are constant residues.

Cyclic Peptides

Many naturally occurring peptides are cyclic. Cyclization is a common mechanism for stabilization of peptide conformation thereby achieving improved association of the peptide with its ligand and hence improved biological activity. Cyclization is usually achieved by intra-chain cystine formation, by formation of peptide bond between side chains or between N- and C- terminals. Cyclization was usually achieved by peptides in solution, but several publications have appeared that describe cyclization of peptides on beads.

A peptide library may be an oligopeptide library or a protein library.

Oligopeptides

Preferably, the oligopeptides are at least five, six, seven or eight amino acids in length. Preferably, they are composed of less than 50, more preferably less than 20 amino acids.

In the case of an oligopeptide library, all or just some of the residues may be variable. The oligopeptide may be unconstrained, or constrained to a particular conformation by, e.g., the participation of constant cysteine residues in the formation of a constraining disulfide bond.

Proteins

Proteins, like oligopeptides, are composed of a plurality of amino acids, but the term protein is usually reserved for longer peptides, which are able to fold into a stable conformation. A protein may be composed of two or more polypeptide chains, held together by covalent or noncovalent crosslinks. These may occur in a homooligomeric

or a heterooligomeric state.

A peptide is considered a protein if it (1) is at least 50 amino acids long, or (2) has at least two stabilizing covalent crosslinks (e.g., disulfide bonds). Thus, conotoxins are considered proteins.

Usually, the proteins of a protein library will be characterizable as having both constant residues (the same for all proteins in the library) and variable residues (which vary from member to member). This is simply because, for a given range of variation at each position, the sequence space (simple diversity) grows exponentially with the number of residue positions, so at some point it becomes inconvenient for all residues of a peptide to be variable positions. Since proteins are usually larger than oligopeptides, it is more common for protein libraries than oligopeptide libraries to feature variable positions.

In the case of a protein library, it is desirable to focus the mutations at those sites which are tolerant of mutation. These may be determined by alanine scanning mutagenesis or by comparison of the protein sequence to that of homologous proteins of similar activity. It is also more likely that mutation of surface residues will directly affect binding. Surface residues may be determined by inspecting a 3D structure of the protein, or by labeling the surface and then ascertaining which residues have received labels. They may also be inferred by identifying regions of high hydrophilicity within the protein.

Because proteins are often altered at some sites but not others, protein libraries can be considered a special case of the biased peptide library.

There are several reasons that one might screen a protein library instead of an oligopeptide library, including (1) a particular protein, mutated in the library, has the desired activity to some degree already, and (2) the oligopeptides are not expected to have a sufficiently high affinity or specificity since they do not have a stable conformation.

When the protein library is based on a parental protein which does not have the desired activity, the parental

protein will usually be one which is of high stability (melting point ≥ 50 deg. C.) and/or possessed of hypervariable regions.

5 The variable domains of an antibody possess hypervariable regions and hence, in some embodiments, the protein library comprises members which comprise a mutant of VH or VL chain, or a mutant of an antigen-specific binding fragment of such a chain. VH and VL chains are usually each about 110 amino acid residues, and are held in proximity by
10 a disulfide bond between the adjoining CL and CH1 regions to form a variable domain. Together, the VH, VL, CL and CH1 form an Fab fragment.

In human heavy chains, the hypervariable regions are at 31-35, 49-65, 98-111 and 84-88, but only the first three are
15 involved in antigen binding. There is variation among VH and VL chains at residues outside the hypervariable regions, but to a much lesser degree.

A sequence is considered a mutant of a VH or VL chain if it is at least 80% identical to a naturally occurring VH
20 or VL chain at all residues outside the hypervariable region.

In a preferred embodiment, such antibody library members comprise both at least one VH chain and at least one VL chain, at least one of which is a mutant chain, and which
25 chains may be derived from the same or different antibodies. The VH and VL chains may be covalently joined by a suitable linker moiety, as in a "single chain antibody", or they may be noncovalently joined, as in a naturally occurring variable domain.

30 If the joining is noncovalent, and the library is displayed on cells or virus, then either the VH or the VL chain may be fused to the carrier surface/coat protein. The complementary chain may be co-expressed, or added exogenously to the library.

35 The members may further comprise some or all of an antibody constant heavy and/or constant light chain, or a mutant thereof.

Peptoid Library

5 A peptoid is an analogue of a peptide in which one or more of the peptide bonds (-NH-CO-) are replaced by pseudopeptide bonds, which may be the same or different. It is not necessary that all of the peptide bonds be replaced, i.e., a peptoid may include one or more conventional amino acid residues, e.g., proline.

10 A peptide bond has two small divalent linker elements, -NH- and -CO-. Thus, a preferred class of pseudopeptide bonds are those which consist of two small divalent linker elements. Each may be chosen independently from the group consisting of amine (-NH-), substituted amine (-NR-), carbonyl (-CO-), thiocarbonyl (-CS-), methylene (-CH₂-), monosubstituted methylene (-CHR-), disubstituted methylene (-CR₁R₂-), ether (-O-) and thioether (-S-). The more
15 preferred pseudopeptide bonds include:

N-modified -NRCO-

Carba Ψ -CH₂-CH₂-

Depsi Ψ -CO-O-

Hydroxyethylene Ψ -CHOH-CH₂-

20 Ketomethylene Ψ -CO-CH₂-

Methylene-Oxy -CH₂-O-

Reduced -CH₂-NH-

Thiomethylene -CH₂-S-

Thiopeptide -CS-NH-

25 Retro-Inverso -CO-NH-

A single peptoid molecule may include more than one kind of pseudopeptide bond.

30 For the purposes of introducing diversity into a peptoid library, one may vary (1) the side chains attached to the core main chain atoms of the monomers linked by the pseudopeptide bonds, and/or (2) the side chains (e.g., the R of an -NRCO-) of the pseudopeptide bonds. Thus, in one embodiment, the monomeric units which are not amino acid
35 residues are of the structure -NR₁-CR₂-CO-, where at least one of R₁ and R₂ are not hydrogen. If there is variability in the pseudopeptide bond, this is most conveniently done by using an -NRCO- or other pseudopeptide bond with an R group, and varying the R group. In this event, the R group will

usually be any of the side chains characterizing the amino acids of peptides, as previously discussed.

If the R group of the pseudopeptide bond is not variable, it will usually be small, e.g., not more than 10 atoms (e.g., hydroxyl, amino, carboxyl, methyl, ethyl, propyl).

If the conjugation chemistries are compatible, a simple combinatorial library may include both peptides and peptoids.

Peptide Nucleic Acid Library

A PNA oligomer is here defined as one comprising a plurality of units, at least one of which is a PNA monomer which comprises a side chain comprising a nucleobase. For nucleobases, see USP 6,077,835.

The classic PNA oligomer is composed of (2-aminoethyl)glycine units, with nucleobases attached by methylene carbonyl linkers. That is, it has the structure



where the outer parenthesized substructure is the PNA monomer.

In this structure, the nucleobase B is separated from the backbone N by three bonds, and the points of attachment of the side chains are separated by six bonds. The nucleobase may be any of the bases included in the nucleotides discussed in connection with oligonucleotide libraries. The bases of nucleotides A, G, T, C and U are preferred.

A PNA oligomer may further comprise one or more amino acid residues, especially glycine and proline.

One can readily envision related molecules in which (1) the $-\text{COCH}_2-$ linker is replaced by another linker, especially one composed of two small divalent linkers as defined previously, (2) a side chain is attached to one of the three main chain carbons not participating in the peptide bond (either instead or in addition to the side chain attached to

the N of the classic PNA); and/or (3) the peptide bonds are replaced by pseudopeptide bonds as disclosed previously in the context of peptoids.

5 PNA oligomer libraries have been made; see e.g. Cook, 6,204,326.

Small Organic Compound Library

10 The small organic compound library ("compound library", for short) is a combinatorial library whose members are suitable for use as drugs if, indeed, they have the ability to mediate a biological activity of the target protein.

15 Peptides have certain disadvantages as drugs. These include susceptibility to degradation by serum proteases, and difficulty in penetrating cell membranes. Preferably, all or most of the compounds of the compound library avoid, or at least do not suffer to the same degree, one or more of the pharmaceutical disadvantages of peptides.

20 In designing a compound library, it is helpful to bear in mind the methods of molecular modification typically used to obtain new drugs. Three basic kinds of modification may be identified: disjunction, in which a lead drug is simplified to identify its component pharmacophoric moieties; conjunction, in which two or more known pharmacophoric moieties, which may be the same or different, are associated, covalently or noncovalently, to form a new drug; and alteration, in which one moiety is replaced by another which may be similar or different, but which is not in effect a disjunction or conjunction. The use of the terms "disjunction", "conjunction" and "alteration" is 30 intended only to connote the structural relationship of the end product to the original leads, and not how the new drugs are actually synthesized, although it is possible that the two are the same.

35 The process of disjunction is illustrated by the evolution of neostigmine (1931) and edrophonium (1952) from physostigmine (1925). Subsequent conjunction is illustrated by demecarium (1956) and ambenonium (1956).

Alterations may modify the size, polarity, or electron distribution of an original moiety. Alterations include

ring closing or opening, formation of lower or higher homologues, introduction or saturation of double bonds, introduction of optically active centers, introduction, removal or replacement of bulky groups, isosteric or
5 bioisosteric substitution, changes in the position or orientation of a group, introduction of alkylating groups, and introduction, removal or replacement of groups with a view toward inhibiting or promoting inductive (electrostatic) or conjugative (resonance) effects.

10 Thus, the substituents may include electron acceptors and/or electron donors. Typical electron donors (+I) include $-\text{CH}_3$, $-\text{CH}_2\text{R}$, $-\text{CHR}_2$, $-\text{CR}_3$ and $-\text{COO}^-$. Typical electron acceptors (-I) include $-\text{NH}_3^+$, $-\text{NR}_3^+$, $-\text{NO}_2$, $-\text{CN}$, $-\text{COOH}$, $-\text{COOR}$, $-\text{CHO}$, $-\text{COR}$, $\frac{\text{R}}{\text{OR}}-\text{COR}$, $-\text{F}$, $-\text{Cl}$, $-\text{Br}$, $-\text{OH}$, $-\text{OR}$, $-\text{SH}$, $-\text{SR}$, $-\text{CH}=\text{CH}_2$,
15 $-\text{CR}=\text{CR}_2$, and $-\text{C}=\text{CH}$.

The substituents may also include those which increase or decrease electronic density in conjugated systems. The former (+R) groups include $-\text{CH}_3$, $-\text{CR}_3$, $-\text{F}$, $-\text{Cl}$, $-\text{Br}$, $-\text{I}$, $-\text{OH}$, $-\text{OR}$, $-\text{OCOR}$, $-\text{SH}$, $-\text{SR}$, $-\text{NH}_2$, $-\text{NR}_2$, and $-\text{NHCOR}$. The later (-R) groups include $-\text{NO}_2$, $-\text{CN}$, $-\text{CHC}$, $-\text{COR}$, $-\text{COOH}$, $-\text{COOR}$, $-\text{CONH}_2$,
20 $-\text{SO}_2\text{R}$ and $-\text{CF}_3$.

Synthetically speaking, the modifications may be achieved by a variety of unit processes, including nucleophilic and electrophilic substitution, reduction and
25 oxidation, addition elimination, double bond cleavage, and cyclization.

For the purpose of constructing a library, a compound, or a family of compounds, having one or more pharmacological activities (which need not be related to the known or
30 suspected activities of the target protein), may be disjoined into two or more known or potential pharmacophoric moieties. Analogues of each of these moieties may be identified, and mixtures of these analogues reacted so as to reassemble compounds which have some similarity to the
35 original lead compound. It is not necessary that all members of the library possess moieties analogous to all of the moieties of the lead compound.

The design of a library may be illustrated by the example of the benzodiazepines. Several benzodiazepine

drugs, including chlordiazepoxide, diazepam and oxazepam, have been used as anti-anxiety drugs. Derivatives of benzodiazepines have widespread biological activities; derivatives have been reported to act not only as anxiolytics, but also as anticonvulsants; cholecystokinin (CCK) receptor subtype A or B, kappa opioid receptor, platelet activating factor, and HIV transactivator Tat antagonists, and GPIIb/IIIa, reverse transcriptase and ras farnesyltransferase inhibitors.

The benzodiazepine structure has been disjoined into a 2-aminobenzophenone, an amino acid, and an alkylating agent. See Bunin, et al., Proc. Nat. Acad. Sci. USA, 91:4708 (1994). Since only a few 2-aminobenzophenone derivatives are commercially available, it was later disjoined into 2-aminoarylstannane, an acid chloride, an amino acid, and an alkylating agent. Bunin, et al., Meth. Enzymol., 267:448 (1996). The arylstannane may be considered the core structure upon which the other moieties are substituted, or all four may be considered equals which are conjoined to make each library member.

A basic library synthesis plan and member structure is shown in Figure 1 of Fowlkes, et al., U.S. Serial No. 08/740,671, incorporated by reference in its entirety. The acid chloride building block introduces variability at the R¹ site. The R² site is introduced by the amino acid, and the R³ site by the alkylating agent. The R⁴ site is inherent in the arylstannane. Bunin, et al. generated a 1, 4-benzodiazepine library of 11,200 different derivatives prepared from 20 acid chlorides, 35 amino acids, and 16 alkylating agents. (No diversity was introduced at R⁴; this group was used to couple the molecule to a solid phase.) According to the Available Chemicals Directory (HDL Information Systems, San Leandro CA), over 300 acid chlorides, 80 Fmoc-protected amino acids and 800 alkylating agents were available for purchase (and more, of course, could be synthesized). The particular moieties used were chosen to maximize structural dispersion, while limiting the numbers to those conveniently synthesized in the wells of a microtiter plate. In choosing between structurally similar

compounds, preference was given to the least substituted compound.

5 The variable elements included both aliphatic and aromatic groups. Among the aliphatic groups, both acyclic and cyclic (mono- or poly-) structures, substituted or not, were tested. (While all of the acyclic groups were linear, it would have been feasible to introduce a branched aliphatic). The aromatic groups featured either single and multiple rings, fused or not, substituted or not, and with 10 heteroatoms or not. The secondary substituents included -NH₂, -OH, -OMe, -CN, -Cl, -F, and -COOH. While not used, spacer moieties, such as -O-, -S-, -OO-, -CS-, -NH-, and -NR-, could have been incorporated.

15 Bunin et al. suggest that instead of using a 1, 4-benzodiazepine as a core structure, one may instead use a 1, 4-benzodiazepine-2, 5-dione structure.

As noted by Bunin et al., it is advantageous, although not necessary, to use a linkage strategy which leaves no trace of the linking functionality, as this permits 20 construction of a more diverse library.

Other combinatorial nonoligomeric compound libraries known or suggested in the art have been based on carbamates, mercaptoacylated pyrrolidines, phenolic agents, aminimides, N-acylamino ethers (made from amino alcohols, aromatic 25 hydroxy acids, and carboxylic acids), N-alkylamino ethers (made from aromatic hydroxy acids, amino alcohols and aldehydes) 1, 4-piperazines, and 1, 4-piperazine-6-ones.

DeWitt, et al., Proc. Nat. Acad. Sci. (USA), 90:6909-13 (1993) describe the simultaneous but separate, synthesis of 30 40 discrete hydantoins and 40 discrete benzodiazepines. They carry out their synthesis on a solid support (inside a gas dispersion tube), in an array format, as opposed to other conventional simultaneous synthesis techniques (e.g., in a well, or on a pin). The hydantoins were synthesized by 35 first simultaneously deprotecting and then treating each of five amino acid resins with each of eight isocyanates. The benzodiazepines were synthesized by treating each of five deprotected amino acid resins with each of eight 2-amino benzophenone imines.

Chen, et al., J. Am. Chem. Soc., 116:2661-62 (1994) described the preparation of a pilot (9 member) combinatorial library of formate esters. A polymer bead-bound aldehyde preparation was "split" into three aliquots, each reacted with one of three different ylide reagents. The reaction products were combined, and then divided into three new aliquots, each of which was reacted with a different Michael donor. Compound identity was found to be determinable on a single bead basis by gas chromatography/mass spectroscopy analysis.

Holmes, USP 5,549,974 (1996) sets forth methodologies for the combinatorial synthesis of libraries of thiazolidinones and metathiazanones. These libraries are made by combination of amines, carbonyl compounds, and thiols under cyclization conditions.

Ellman, USP 5,545,568 (1996) describes combinatorial synthesis of benzodiazepines, prostaglandins, beta-turn mimetics, and glycerol-based compounds. See also Ellman, USP 5,288,514.

Summerton, USP 5,506,337 (1996) discloses methods of preparing a combinatorial library formed predominantly of morpholino subunit structures.

Heterocyclic combinatorial libraries are reviewed generally in Nefzi, et al., Chem. Rev., 97:449-472 (1997).

For pharmacological classes, see, e.g., Goth, Medical Pharmacology: Principles and Concepts (C.V. Mosby Co.: 8th ed. 1976); Korolkovas and Burckhalter, Essentials of Medicinal Chemistry (John Wiley & Sons, Inc.: 1976). For synthetic methods, see, e.g., Warren, Organic Synthesis: The Disconnection Approach (John Wiley & Sons, Ltd.: 1982); Fuson, Reactions of Organic Compounds (John Wiley & Sons: 1966); Payne and Payne, How to do an Organic Synthesis (Allyn and Bacon, Inc.: 1969); Greene, Protective Groups in Organic Synthesis (Wiley-Interscience). For selection of substituents, see e.g., Hansch and Leo, Substituent Constants for Correlation Analysis in Chemistry and Biology (John Wiley & Sons: 1979).

The library is preferably synthesized so that the

individual members remain identifiable so that, if a member is shown to be active, it is not necessary to analyze it. . . Several methods of identification have been proposed, including:

- 5 (1) encoding, i.e., the attachment to each member of an identifier moiety which is more readily identified than the member proper. This has the disadvantage that the tag may itself influence the activity of the conjugate.
- 10 (2) spatial addressing, e.g., each member is synthesized only at a particular coordinate on or in a matrix, or in a particular chamber. This might be, for example, the location of a particular pin, or a particular well on a
- 15 microtiter plate, or inside a "tea bag".

The present invention is not limited to any particular form of identification.

However, it is possible to simply characterize those members of the library which are found to be active, based on the characteristic spectroscopic indicia of the various building blocks.

Solid phase synthesis permits greater control over which derivatives are formed. However, the solid phase could interfere with activity. To overcome this problem, some or all of the molecules of each member could be

25 liberated, after synthesis but before screening.

Examples of candidate simple libraries which might be evaluated include derivatives of the following:

Cyclic Compounds Containing One Hetero Atom

30 Heteronitrogen

pyrroles

pentasubstituted pyrroles

pyrrolidines

pyrrolines

35 prolines

indoles

beta-carbolines

pyridines

dihydropyridines

- 1,4-dihydropyridines
- pyrido[2,3-d]pyrimidines
- tetrahydro-3H-imidazo[4,5-c] pyridines
- Isoquinolines
- 5 tetrahydroisoquinolines
- quinolones
- beta-lactams
- azabicyclo[4.3.0]nonen-8-one amino acid
- Heterooxygen
- 10 furans
- tetrahydrofurans
- 2,5-disubstituted tetrahydrofurans
- pyrans
- hydroxypyranones
- 15 tetrahydroxypyranones
- gamma-butyrolactones
- Heterosulfur
- sulfolenes
- Cyclic Compounds with Two or More Hetero atoms
- 20 Multiple heteronitrogens
- imidazoles
- pyrazoles
- piperazines
- diketopiperazines
- 25 arylpiperazines
- benzylpiperazines
- benzodiazepines
- 1,4-benzodiazepine-2,5-diones
- hydantoins
- 30 5-alkoxyhydantoins
- dihydropyrimidines
- 1,3-disubstituted-5,6-dihydropyrimidine-2,4-diones
- 35 cyclic ureas
- cyclic thioureas
- quinazolines
- chiral 3-substituted-quinazoline-2,4-diones

triazoles
1,2,3-triazoles
purines
Heteronitrogen and Heterooxygen
dikelomorpholines
isoxazoles
isoxazolines
Heteronitrogen and Heterosulfur
thiazolidines
N-axylthiazolidines
dihydrothiazoles
2-methylene-2,3-dihydrothiazates
2-aminothiazoles
thiophenes
3-amino thiophenes
4-thiazolidinones
4-melathiazanones
benzisothiazolones

For details on synthesis of libraries, see Nefzi, et al., Chem. Rev., 97:449-72 (1997), and references cited therein.

Pharmaceutical Methods and Preparations

The preferred animal subject of the present invention is a mammal. By the term "mammal" is meant an individual belonging to the class Mammalia. The invention is particularly useful in the treatment of human subjects, although it is intended for veterinary and nutritional uses as well. Preferred nonhuman subjects are of the orders Primata (e.g., apes and monkeys), Artiodactyla or Perissodactyla (e.g., cows, pigs, sheep, horses, goats), Carnivora (e.g., cats, dogs), Rodenta (e.g., rats, mice, guinea pigs, hamsters), Lagomorpha (e.g., rabbits) or other pet, farm or laboratory mammals.

The term "protection", as used herein, is intended to include "prevention," "suppression" and "treatment." "Prevention", strictly speaking, involves administration of the pharmaceutical prior to the induction of the disease (or other adverse clinical condition). "Suppression" involves

administration of the composition prior to the clinical appearance of the disease. "Treatment" involves administration of the protective composition after the appearance of the disease.

5 It will be understood that in human and veterinary medicine, it is not always possible to distinguish between "preventing" and "suppressing" since the ultimate inductive event or events may be unknown, latent, or the patient is not ascertained until well after the occurrence of the event
10 or events. Therefore, unless qualified, the term "prevention" will be understood to refer to both prevention in the strict sense, and to suppression.

The preventative or prophylactic use of a pharmaceutical usually involves identifying subjects who are
15 at higher risk than the general population of contracting the disease, and administering the pharmaceutical to them in advance of the clinical appearance of the disease. The effectiveness of such use is measured by comparing the subsequent incidence or severity of the disease, or of
20 particular symptoms of the disease, in the treated subjects against that in untreated subjects of the same high risk group.

While high risk factors vary from disease to disease, in general, these include (1) prior occurrence of the
25 disease in one or more members of the same family, or, in the case of a contagious disease, in individuals with whom the subject has come into potentially contagious contact at a time when the earlier victim was likely to be contagious, (2) a prior occurrence of the disease in the subject, (3)
30 prior occurrence of a related disease, or a condition known to increase the likelihood of the disease, in the subject; (4) appearance of a suspicious level of a marker of the disease, or a related disease or condition; (5) a subject who is immunologically compromised, e.g., by radiation
35 treatment, HIV infection, drug use,, etc., or (6) membership in a particular group (e.g., a particular age, sex, race, ethnic group, etc.) which has been epidemiologically associated with that disease.

In some cases, it may be desirable to provide

prophylaxis for the general population, and not just a high risk group. This is most likely to be the case when essentially all are at risk of contracting the disease, the effects of the disease are serious, the therapeutic index of the prophylactic agent is high, and the cost of the agent is low.

A prophylaxis or treatment may be curative, that is, directed at the underlying cause of a disease, or ameliorative, that is, directed at the symptoms of the disease, especially those which reduce the quality of life.

It should also be understood that to be useful, the protection provided need not be absolute, provided that it is sufficient to carry clinical value. An agent which provides protection to a lesser degree than do competitive agents may still be of value if the other agents are ineffective for a particular individual, if it can be used in combination with other agents to enhance the level of protection, or if it is safer than competitive agents. It is desirable that there be a statistically significant ($p=0.05$ or less) improvement in the treated subject relative to an appropriate untreated control, and it is desirable that this improvement be at least 10%, more preferably at least 25%, still more preferably at least 50%, even more preferably at least 100%, in some indicia of the incidence or severity of the disease or of at least one symptom of the disease.

At least one of the drugs of the present invention may be administered, by any means that achieve their intended purpose, to protect a subject against a disease or other adverse condition. The form of administration may be systemic or topical. For example, administration of such a composition may be by various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, transdermal, or buccal routes. Alternatively, or concurrently, administration may be by the oral route. Parenteral administration can be by bolus injection or by gradual perfusion over time.

A typical regimen comprises administration of an effective amount of the drug, administered over a period ranging from a single dose, to dosing over a period of

hours, days, weeks, months, or years.

It is understood that the suitable dosage of a drug of the present invention will be dependent upon the age, sex, health, and weight of the recipient, kind of concurrent
5 treatment, if any, frequency of treatment, and the nature of the effect desired. However, the most preferred dosage can be tailored to the individual subject, as is understood and determinable by one of skill in the art, without undue experimentation. This will typically involve adjustment of
10 a standard dose, e.g., reduction of the dose if the patient has a low body weight.

Prior to use in humans, a drug will first be evaluated for safety and efficacy in laboratory animals. In human clinical studies, one would begin with a dose expected to be
15 safe in humans, based on the preclinical data for the drug in question, and on customary doses for analogous drugs (if any). If this dose is effective, the dosage may be decreased, to determine the minimum effective dose, if desired. If this dose is ineffective, it will be cautiously
20 increased, with the patients monitored for signs of side effects. See, e.g., Berkow et al, eds., *The Merck Manual*, 15th edition, Merck and Co., Rahway, N.J., 1987; Goodman et al., eds., *Goodman and Gilman's The Pharmacological Basis of Therapeutics*, 8th edition, Pergamon Press, Inc., Elmsford,
25 N.Y., (1990); *Avery's Drug Treatment: Principles and Practice of Clinical Pharmacology and Therapeutics*, 3rd edition, ADIS Press, LTD., Williams and Wilkins, Baltimore, MD. (1987), Ebadi, *Pharmacology*, Little, Brown and Co., Boston, (1985), which references and references cited
30 therein, are entirely incorporated herein by reference.

The total dose required for each treatment may be administered by multiple doses or in a single dose. The protein may be administered alone or in conjunction with other therapeutics directed to the disease or directed to
35 other symptoms thereof.

Typical pharmaceutical doses, for adult humans, are in the range of 1 ng to 10g per day, more often 1 mg to 1g per day.

The appropriate dosage form will depend on the disease,

the pharmaceutical, and the mode of administration; possibilities include tablets, capsules, lozenges, dental pastes, suppositories, inhalants, solutions, ointments and parenteral depots. See, e.g., Berker, *supra*, Goodman, *supra*, Avery, *supra* and Ebadi, *supra*, which are entirely incorporated herein by reference, including all references cited therein.

In the case of peptide drugs, the drug may be administered in the form of an expression vector comprising a nucleic acid encoding the peptide; such a vector, after incorporation into the genetic complement of a cell of the patient, directs synthesis of the peptide. Suitable vectors include genetically engineered poxviruses (vaccinia), adenoviruses, adeno-associated viruses, herpesviruses and lentiviruses which are or have been rendered nonpathogenic.

In addition to at least one drug as described herein, a pharmaceutical composition may contain suitable pharmaceutically acceptable carriers, such as excipients, carriers and/or auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. See, e.g., Berker, *supra*, Goodman, *supra*, Avery, *supra* and Ebadi, *supra*, which are entirely incorporated herein by reference, included all references cited therein.

Assay Compositions and Methods

Target Organism

The invention contemplates that it may be appropriate to ascertain or to mediate the biological activity of a substance of this invention in a target organism.

The target organism may be a plant, animal, or microorganism.

In the case of a plant, it may be an economic plant, in which case the drug may be intended to increase the disease, weather or pest resistance, alter the growth characteristics, or otherwise improve the useful characteristics or mute undesirable characteristics of the plant. Or it may be a weed, in which case the drug may be intended to kill or otherwise inhibit the growth of the

plant, or to alter its characteristics to convert it from a weed to an economic plant. The plant may be a tree, shrub, crop, grass, etc. The plant may be an algae (which are in some cases also microorganisms), or a vascular plant, especially gymnosperms (particularly conifers) and angiosperms. Angiosperms may be monocots or dicots. The plants of greatest interest are rice, wheat, corn, alfalfa, soybeans, potatoes, peanuts, tomatoes, melons, apples, pears, plums, pineapples, fir, spruce, pine, cedar, and oak.

If the target organism is a microorganism, it may be algae, bacteria, fungi, or a virus (although the biological activity of a virus must be determined in a virus-infected cell). The microorganism may be human or other animal or plant pathogen, or it may be nonpathogenic. It may be a soil or water organism, or one which normally lives inside other living things.

If the target organism is an animal, it may be a vertebrate or a nonvertebrate animal. Nonvertebrate animals are chiefly of interest when they act as pathogens or parasites, and the drugs are intended to act as biocidal or biostatic agents. Nonvertebrate animals of interest include worms, mollusks, and arthropods.

The target organism may also be a vertebrate animal, i.e., a mammal, bird, reptile, fish or amphibian. Among mammals, the target animal preferably belongs to the order Primata (humans, apes and monkeys), Artiodactyla (e.g., cows, pigs, sheep, goats, horses), Rodenta (e.g., mice, rats) Lagomorpha (e.g., rabbits, hares), or Carnivora (e.g., cats, dogs). Among birds, the target animals are preferably of the orders Anseriformes (e.g., ducks, geese, swans) or Galliformes (e.g., quails, grouse, pheasants, turkeys and chickens). Among fish, the target animal is preferably of the order Clupeiformes (e.g., sardines, shad, anchovies, whitefish, salmon).

Target Tissues

The term "target tissue" refers to any whole animal, physiological system, whole organ, part of organ, miscellaneous tissue, cell, or cell component (e.g., the

cell membrane) of a target animal in which biological activity may be measured.

Routinely in mammals one would choose to compare and contrast the biological impact on virtually any and all tissues which express the subject receptor protein. The main tissues to use are: brain, heart, lung, kidney, liver, pancreas, skin, intestines, adipose, stomach, skeletal muscle, adrenal glands, breast, prostate, vasculature, retina, cornea, thyroid gland, parathyroid glands, thymus, bone marrow, bone, etc.

Another classification would be by cell type: B cells, T cells, macrophages, neutrophils, eosinophils, mast cells, platelets, megakaryocytes, erythrocytes, bone marrow stomal cells, fibroblasts, neurons, astrocytes, neuroglia, microglia, epithelial cells (from any organ, e.g. skin, breast, prostate, lung, intestines etc), cardiac muscle cells, smooth muscle cells, striated muscle cells, osteoblasts, osteocytes, chondroblasts, chondrocytes, keratinocytes, melanocytes, etc.

Of course, in the case of a unicellular organism, there is no distinction between the "target organism" and the "target tissue".

Screening Assays

Assays intended to determine the binding or the biological activity of a substance are called preliminary screening assays.

Screening assays will typically be either in vitro (cell-free) assays (for binding to an immobilized receptor) or cell-based assays (for alterations in the phenotype of the cell). They will not involve screening of whole multicellular organisms, or isolated organs. The comments on diagnostic biological assays apply mutatis mutandis to screening cell-based assays.

In Vitro vs. In Vivo Assays

The term *in vivo* is descriptive of an event, such as binding or enzymatic action, which occurs within a living organism. The organism in question may, however, be

genetically modified. The term *in vitro* refers to an event which occurs outside a living organism. Parts of an organism (e.g., a membrane, or an isolated biochemical) are used, together with artificial substrates and/or conditions. For the purpose of the present invention, the term *in vitro* excludes events occurring inside or on an intact cell, whether of a unicellular or multicellular organism.

In vivo assays include both cell-based assays, and organismic assays. The cell-based assays include both assays on unicellular organisms, and assays on isolated cells or cell cultures derived from multicellular organisms. The cell cultures may be mixed, provided that they are not organized into tissues or organs. The term organismic assay refers to assays on whole multicellular organisms, and assays on isolated organs or tissues of such organisms.

In vitro Diagnostic Methods and Reagents

The *in vitro* assays of the present invention may be applied to any suitable analyte-containing sample, and may be qualitative or quantitative in nature.

Sample

The sample will normally be a biological fluid, such as blood, urine, lymph, semen, milk, or cerebrospinal fluid, or a fraction or derivative thereof, or a biological tissue, in the form of, e.g., a tissue section or homogenate. However, the sample conceivably could be (or derived from) a food or beverage, a pharmaceutical or diagnostic composition, soil, or surface or ground water. If a biological fluid or tissue, it may be taken from a human or other mammal, vertebrate or animal, or from a plant. The preferred sample is blood, or a fraction or derivative thereof.

Binding and Reaction Assays

The assay may be a binding assay, in which one step involves the binding of a diagnostic reagent to the analyte, or a reaction assay, which involves the reaction of a reagent with the analyte. The reagents used in a binding

assay may be classified as to the nature of their interaction with analyte: (1) analyte analogues, or (2) analyte binding molecules (ABM). They may be labeled or insolubilized.

5 In a reaction assay, the assay may look for a direct reaction between the analyte and a reagent which is reactive with the analyte, or if the analyte is an enzyme or enzyme inhibitor, for a reaction catalyzed or inhibited by the analyte. The reagent may be a reactant, a catalyst, or an
10 inhibitor for the reaction.

An assay may involve a cascade of steps in which the product of one step acts as the target for the next step. These steps may be binding steps, reaction steps, or a combination thereof.

15 *Signal Producing System (SPS)*

In order to detect the presence, or measure the amount, of an analyte, the assay must provide for a signal producing
20 system (SPS) in which there is a detectable difference in the signal produced, depending on whether the analyte is present or absent (or, in a quantitative assay, on the amount of the analyte). The detectable signal may be one which is visually detectable, or one detectable only with
25 instruments. Possible signals include production of colored or luminescent products, alteration of the characteristics (including amplitude or polarization) of absorption or emission of radiation by an assay component or product, and precipitation or agglutination of a component or product.
30 The term "signal" is intended to include the discontinuance of an existing signal, or a change in the rate of change of an observable parameter, rather than a change in its absolute value. The signal may be monitored manually or automatically.

35 In a reaction assay, the signal is often a product of the reaction. In a binding assay, it is normally provided by a label borne by a labeled reagent.

The component of the signal producing system which is most intimately associated with the diagnostic reagent is called the "label". A label may be, e.g., a radioisotope, a fluorophore, an enzyme, a co-enzyme, an enzyme substrate, an electron-dense compound, an agglutinable particle.

The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography. Isotopes which are particularly useful for the purpose of the present invention include ^3H , ^{125}I , ^{131}I , ^{35}S , ^{14}C , ^{32}P and ^{33}P . ^{125}I is preferred for antibody labeling.

The label may also be a fluorophore. When the fluorescently labeled reagent is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, α -phthaldehyde and fluorescamine.

Alternatively, fluorescence-emitting metals such as ^{125}Eu , or others of the lanthanide series, may be incorporated into a diagnostic reagent using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediamine-tetraacetic acid (EDTA).

The label may also be a chemiluminescent compound. The presence of the chemiluminescently labeled reagent is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isolumino, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used for labeling. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Enzyme labels, such as horseradish peroxidase and

alkaline phosphatase, are preferred. When an enzyme label is used, the signal producing system must also include a substrate for the enzyme. If the enzymatic reaction product is not itself detectable, the SPS will include one or more additional reactants so that a detectable product appears.

An enzyme analyte may act as its own label if an enzyme inhibitor is used as a diagnostic reagent.

Binding Assay Formats

Binding assays may be divided into two basic types, heterogeneous and homogeneous. In heterogeneous assays, the interaction between the affinity molecule and the analyte does not affect the label, hence, to determine the amount or presence of analyte, bound label must be separated from free label. In homogeneous assays, the interaction does affect the activity of the label, and therefore analyte levels can be deduced without the need for a separation step.

In one embodiment, the ABM is insolubilized by coupling it to a macromolecular support, and analyte in the sample is allowed to compete with a known quantity of a labeled or specifically labelable analyte analogue. The "analyte analogue" is a molecule capable of competing with analyte for binding to the ABM, and the term is intended to include analyte itself. It may be labeled already, or it may be labeled subsequently by specifically binding the label to a moiety differentiating the analyte analogue from analyte. The solid and liquid phases are separated, and the labeled analyte analogue in one phase is quantified. The higher the level of analyte analogue in the solid phase, i.e., sticking to the ABM, the lower the level of analyte in the sample.

In a "sandwich assay", both an insolubilized ABM, and a labeled ABM are employed. The analyte is captured by the insolubilized ABM and is tagged by the labeled ABM, forming a ternary complex. The reagents may be added to the sample in either order, or simultaneously. The ABMs may be the same or different. The amount of labeled ABM in the ternary complex is directly proportional to the amount of analyte in the sample.

The two embodiments described above are both heterogeneous assays. However, homogeneous assays are conceivable. The key is that the label be affected by whether or not the complex is formed.

5 **Conjugation Methods**

A label may be conjugated, directly or indirectly (e.g., through a labeled anti-ABM antibody), covalently (e.g., with SPDP) or noncovalently, to the ABM, to produce a diagnostic reagent. Similarly, the ABM may be conjugated to
10 a solid phase support to form a solid phase ("capture") diagnostic reagent.

Suitable supports include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses,
15 and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention.

The support material may have virtually any possible structural configuration so long as the coupled molecule is
20 capable of binding to its target. Thus the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc.

25

Biological Assays

A biological assay measures or detects a biological response of a biological entity to a substance.

The biological entity may be a whole organism, an
30 isolated organ or tissue, freshly isolated cells, an immortalized cell line, or a subcellular component (such as a membrane; this term should not be construed as including an isolated receptor). The entity may be, or may be derived from, an organism which occurs in nature, or which is
35 modified in some way. Modifications may be genetic (including radiation and chemical mutants, and genetic engineering) or somatic (e.g., surgical, chemical, etc.). In the case of a multicellular entity, the modifications may affect some or all cells. The entity need not be the target

organism, or a derivative thereof, if there is a reasonable correlation between bioassay activity in the assay entity and biological activity in the target organism.

5 The entity is placed in a particular environment, which may be more or less natural. For example, a culture medium may, but need not, contain serum or serum substitutes, and it may, but need not, include a support matrix of some kind, it may be still, or agitated. It may contain particular biological or chemical agents, or have particular physical
10 parameters (e.g., temperature), that are intended to nourish or challenge the biological entity.

There must also be a detectable biological marker for the response. At the cellular level, the most common markers are cell survival and proliferation, cell behavior²⁸
15 (clustering, motility), cell morphology (shape, color), and biochemical activity (overall DNA synthesis, overall protein synthesis, and specific metabolic activities, such as utilization of particular nutrients, e.g., consumption of oxygen, production of CO₂, production of organic acids,
20 uptake or discharge of ions).

The direct signal produced by the biological marker may be transformed by a signal producing system into a different signal which is more observable, for example, a fluorescent or colorimetric signal.

25 The entity, environment, marker and signal producing system are chosen to achieve a clinically acceptable level of sensitivity, specificity and accuracy.

In some cases, the goal will be to identify substances which mediate the biological activity of a natural
30 biological entity, and the assay is carried out directly with that entity. In other cases, the biological entity is used simply as a model of some more complex (or otherwise inconvenient to work with) biological entity. In that event, the model biological entity is used because activity
35 in the model system is considered more predictive of activity in the ultimate natural biological entity than is simple binding activity in an in vitro system. The model entity is used instead of the ultimate entity because the former is more expensive or slower to work with, or because

ethical considerations forbid working with the ultimate entity yet.

5 The model entity may be naturally occurring, if the model entity usefully models the ultimate entity under some conditions. Or it may be non-naturally occurring, with modifications that increase its resemblance to the ultimate entity.

Transgenic animals, such as transgenic mice, rats, and rabbits, have been found useful as model systems.

10 In cell-based model assays, where the biological activity is mediated by binding to a receptor (target protein), the receptor may be functionally connected to a signal (biological marker) producing system, which may be endogenous or exogenous to the cell.

15 There are a number of techniques of doing this.

"Zero-Hybrid" Systems

20 In these systems, the binding of a peptide to the target protein results in a screenable or selectable phenotypic change, without resort to fusing the target protein (or a ligand binding moiety thereof) to an endogenous protein. It may be that the target protein is endogenous to the host cell, or is substantially identical to an endogenous receptor so that it can take advantage of
25 the latter's native signal transduction pathway. Or sufficient elements of the signal transduction pathway normally associated with the target protein may be engineered into the cell so that the cell signals binding to the target protein.

30

"One-Hybrid" Systems

35 In these systems, a chimera receptor, a hybrid of the target protein and an endogenous receptor, is used. The chimeric receptor has the ligand binding characteristics of the target protein and the signal transduction characteristics of the endogenous receptor. Thus, the normal signal transduction pathway of the endogenous receptor is subverted.

Preferably, the endogenous receptor is inactivated, or

the conditions of the assay avoid activation of the endogenous receptor, to improve the signal-to-noise ratio.

See Fowlkes USP 5,789,184 for a yeast system.

- Another type of "one-hybrid" system combines a peptide:
5 DNA-binding domain fusion with an unfused target receptor that possesses an activation domain.

"Two-Hybrid" System

- In a preferred embodiment, the cell-based assay is a
10 two hybrid system. This term implies that the ligand is incorporated into a first hybrid protein, and the receptor into a second hybrid protein. The first hybrid also comprises component A of a signal generating system, and the second hybrid comprises component B of that system.
15 Components A and B, by themselves, are insufficient to generate a signal. However, if the ligand binds the receptor, components A and B are brought into sufficiently close proximity so that they can cooperate to generate a signal.

- 20 Components A and B may naturally occur, or be substantially identical to moieties which naturally occur, as components of a single naturally occurring biomolecule, or they may naturally occur, or be substantially identical to moieties which naturally occur, as separate naturally
25 occurring biomolecules which interact in nature.

Two-Hybrid System: Transcription Factor Type

- In a preferred "two-hybrid" embodiment, one member of a peptide ligand:receptor binding pair is expressed as a
30 fusion to a DNA-binding domain (DBD) from a transcription factor (this fusion protein is called the "bait"), and the other is expressed as a fusion to a transactivation domain (TAD) (this fusion protein is called the "fish", the "prey", or the "catch"). The transactivation domain should be
35 complementary to the DNA-binding domain, i.e., it should interact with the latter so as to activate transcription of a specially designed reporter gene that carries a binding site for the DNA-binding domain. Naturally, the two fusion proteins must likewise be complementary.

This complementarity may be achieved by use of the complementary and separable DNA-binding and transcriptional activator domains of a single transcriptional activator protein, or one may use complementary domains derived from different proteins. The domains may be identical to the native domains, or mutants thereof. The assay members may be fused directly to the DBD or TAD, or fused through an intermediated linker.

The target DNA operator may be the native operator sequence, or a mutant operator. Mutations in the operator may be coordinated with mutations in the DBD and the TAD. An example of a suitable transcription activation system is one comprising the DNA-binding domain from the bacterial repressor LexA and the activation domain from the yeast transcription factor Gal4, with the reporter gene operably linked to the LexA operator.

It is not necessary to employ the intact target receptor; just the ligand-binding moiety is sufficient.

The two fusion proteins may be expressed from the same or different vectors. Likewise, the activatable reporter gene may be expressed from the same vector as either fusion protein (or both proteins), or from a third vector.

Potential DNA-binding domains include Gal4, LexA, and mutant domains substantially identical to the above.

Potential activation domains include E. coli B42, Gal4 activation domain II, and HSV VP16, and mutant domains substantially identical to the above.

Potential operators include the native operators for the desired activation domain, and mutant domains substantially identical to the native operator.

The fusion proteins may comprise nuclear localization signals.

The assay system will include a signal producing system, too. The first element of this system is a reporter gene operably linked to an operator responsive to the DBD and TAD of choice. The expression of this reporter gene will result, directly or indirectly, in a selectable or screenable phenotype (the signal). The signal producing system may include, besides the reporter gene, additional

genetic or biochemical elements which cooperate in the production of the signal. Such an element could be, for example, a selective agent in the cell growth medium. There may be more than one signal producing system, and the system
5 may include more than one reporter gene.

The sensitivity of the system may be adjusted by, e.g., use of competitive inhibitors of any step in the activation or signal production process, increasing or decreasing the number of operators, using a stronger or weaker DBD or TAD,
10 etc.

When the signal is the death or survival of the cell in question, or proliferation or nonproliferation of the cell in question, the assay is said to be a selection. When the signal merely results in a detectable phenotype by which the
15 signaling cell may be differentiated from the same cell in a nonsignaling state (either way being a living cell), the assay is a screen. However, the term "screening assay" may be used in a broader sense to include a selection. When the narrower sense is intended, we will use the term
20 "nonselective screen".

Various screening and selection systems are discussed in Ladner, USP 5,198,346.

Screening and selection may be for or against the peptide: target protein or compound:target protein
25 interaction.

Preferred assay cells are microbial (bacterial, yeast, algal, protozoal), invertebrate, vertebrate (esp. mammalian, particularly human). The best developed two-hybrid assays are yeast and mammalian systems.

30 Normally, two hybrid assays are used to determine whether a protein X and a protein Y interact, by virtue of their ability to reconstitute the interaction of the DBD and the TAD. However, augmented two-hybrid assays have been used to detect interactions that depend on a third, non-
35 protein ligand.

For more guidance on two-hybrid assays, see Brent and Finley, Jr., Ann. Rev. Genet., 31:663-704 (1997); Fremont-Racine, et al., Nature Genetics, 277-281 (16 July 1997); Allen, et al., TIBS, 511-16 (Dec. 1995); LeCrenier, et al.,

BioEssays, 20:1-6 (1998); Xu, et al., Proc. Nat. Acad. sci. (USA), 94:12473-8 (Nov. 1992); Esotak, et al., Mol. Cell. Biol., 15:5820-9 (1995); Yang, et al., Nucleic Acids Res., 23:1152-6 (1995); Bendixen, et al., Nucleic Acids Res., 22:1778-9 (1994); Fuller, et al., BioTechniques, 25:85-92 (July 1998); Cohen, et al., PNAS (USA) 95:14272-7 (1998); Kolonin and Finley, Jr., PNAS (USA) 95:14266-71 (1998). See also Vasavada, et al., PNAS (USA), 88:10686-90 (1991) (contingent replication assay), and Rehrauer, et al., J. Biol. Chem., 271:23865-73 (1996) (LexA repressor cleavage assay).

Two-Hybrid Systems: reporter Enzyme type

In another embodiment, the components A and B reconstitute an enzyme which is not a transcription factor.

As in the last example, the effect of the reconstitution of the enzyme is a phenotypic change which may be a screenable change, a selectable change, or both.

In vivo Diagnostic Uses

Radio-labeled ABM may be administered to the human or animal subject. Administration is typically by injection, e.g., intravenous or arterial or other means of administration in a quantity sufficient to permit subsequent dynamic and/or static imaging using suitable radio-detecting devices. The dosage is the smallest amount capable of providing a diagnostically effective image, and may be determined by means conventional in the art, using known radio-imaging agents as a guide.

Typically, the imaging is carried out on the whole body of the subject, or on that portion of the body or organ relevant to the condition or disease under study. The amount of radio-labeled ABM accumulated at a given point in time in relevant target organs can then be quantified.

A particularly suitable radio-detecting device is a scintillation camera, such as a gamma camera. A scintillation camera is a stationary device that can be used to image distribution of radio-labeled ABM. The detection

device in the camera senses the radioactive decay, the distribution of which can be recorded. Data produced by the imaging system can be digitized. The digitized information can be analyzed over time discontinuously or continuously.

5 The digitized data can be processed to produce images, called frames, of the pattern of uptake of the radio-labeled ABM in the target organ at a discrete point in time. In most continuous (dynamic) studies, quantitative data is obtained by observing changes in distributions of

10 radioactive decay in target organs over time. In other words, a time-activity analysis of the data will illustrate uptake through clearance of the radio-labeled binding protein by the target organs with time.

Various factors should be taken into consideration in selecting an appropriate radioisotope. The radioisotope must be selected with a view to obtaining good quality resolution upon imaging, should be safe for diagnostic use in humans and animals, and should preferably have a short physical half-life so as to decrease the amount of radiation received by the body. The radioisotope used should preferably be pharmacologically inert, and, in the quantities administered, should not have any substantial physiological effect.

The ABM may be radio-labeled with different isotopes of iodine, for example ^{123}I , ^{125}I , or ^{131}I (see for example, U.S. Patent 4,609,725). The extent of radio-labeling must, however be monitored, since it will affect the calculations made based on the imaging results (i.e. a diiodinated ABM will result in twice the radiation count of a similar moniodinated ABM over the same time frame).

In applications to human subjects, it may be desirable to use radioisotopes other than ^{125}I for labeling in order to decrease the total dosimetry exposure of the human body and to optimize the detectability of the labeled molecule (though this radioisotope can be used if circumstances require). Ready availability for clinical use is also a factor. Accordingly, for human applications, preferred radio-labels are for example, $^{99\text{m}}\text{Tc}$, ^{67}Ga , ^{68}Ga , ^{90}Y , ^{111}In , $^{113\text{m}}\text{In}$, ^{123}I , ^{186}Re , ^{188}Re or ^{211}At .

The radio-labeled ABM may be prepared by various methods. These include radio-halogenation by the chloramine - T method or the lactoperoxidase method and subsequent purification by HPLC (high pressure liquid chromatography), for example as described by J. Gutkowska et al in "Endocrinology and Metabolism Clinics of America: (1987) 16 (1):183. Other known methods of radio-labeling can be used, such as IODOBEADS™.

There are a number of different methods of delivering the radio-labeled ABM to the end-user. It may be administered by any means that enables the active agent to reach the agent's site of action in the body of a mammal. Because proteins are subject to being digested when administered orally, parenteral administration, i.e., intravenous, subcutaneous, intramuscular, would ordinarily be used to optimize absorption of an ABM, such as an antibody, which is a protein.

EXAMPLES

We are utilizing a mouse model of diet-induced obesity that progresses to diabetes. The diet is high in fat and has been documented to lead to diabetes in C57BL/6J mice (Surwit et al., 1988). After weaning, C57BL/6J mice were fed either the high fat diet or a standard lab chow diet for 16 weeks. Body weight was monitored bi-weekly. Fasting glucose and insulin levels were measured after 2, 4, 8, and 16 weeks on the diets. At each time point, several diabetic and control mice were sacrificed and a number of tissues collected. For further analysis, RNA was extracted from the pancreas at each time point and used in DNA microarray analyses.

Animal Models.

Obesity and subsequent hyperinsulinemia and hyperglycemia were induced by feeding a group of 3 week old mice (50 C57BL/6 males) a high-fat diet (Bio-Serve, Frenchtown, NJ, #F1850 High Carbohydrate-High Fat; 56% of calories from fat, 16% from protein and 27% from carbohydrates). Another group of 3 week old mice (20 C57BL/6 males) were fed the normal control diet (PMI Nutrition International Inc., Brentwood, MO, Prolab RMH3000; 14% of calories from fat, 16% from protein and 60% from carbohydrates). The mice were placed onto the respective diets immediately following weaning. Animal weights were determined weekly. Fasting blood-glucose and plasma insulin measurements were determined after 2, 4, 8 and 16 weeks on the respective diets.

Normal weight, normal fasting blood glucose and normal fasting plasma insulin levels are defined as the respective mean values of the animals fed the control diet.

Two of the "most typical" animals were selected for each group (Control, hyperinsulinemic and Diabetic) at each time point (2, 4, 8, and 16 weeks after commencement of diet) for sacrifice. The selected mice were sacrificed and pancreas tissue obtained and immediately processed for RNA isolation.

Fasting Blood Glucose Levels.

The day after obtaining body weight measurements at the indicated time points (top panel), mice were fasted 8 hours and blood glucose levels was measured from a drop of blood taken from the tip of the tail of fasted (8 hr) mice using a Lifescan Genuine One Touch glucometer. All measurements occurred between 2:00 pm and 5:00 pm.

Plasma insulin measurements.

Blood was collected from the tail of fasted (8 hr) mice into a heparinized capillary tube and stored on ice. All collections occurred between 2:00 pm and 5:00 pm. Plasma was separated from red blood cells by centrifugation for 10 minutes at 8000 x g and then stored at -20°C. Insulin concentrations were determined using the Ultra-Sensitive Rat Insulin ELISA kit (ALPCO) and rat insulin standards (ALPCO) essentially as instructed by the manufacturer. Values were adjusted by a factor of 1.23 as determined by the manufacturer to correct for the species difference in cross-reactivity with the antibody.

RNA isolation.

Total RNA was isolated from pancreas using the RNA STAT-60 Total RNA/mRNA Isolation Reagent according to the manufacturer's instructions (Tel-Test, Friendswood, TX).

Sample Quantification and Quality Assessment

Total RNA was quantified and assessed for quality on a Bioanalyzer RNA 6000 Nano chip (Agilent). Each chip contained an interconnected set of gel-filled channels that allowed for molecular sieving of nucleic acids. Pin-electrodes in the chip were used to create electrokinetic forces capable of driving molecules through these micro-channels to perform electrophoretic separations. Ribosomal peaks were measured by fluorescence signal and displayed in an electropherogram. A successful total RNA sample featured 2 distinct ribosomal peaks (18S and 28S rRNA).

Biotinylated cRNA Hybridization Target.

Total RNA was prepared for use as a hybridization target as described in the manufacturer's instructions for CodeLink Expression Bioarrays(TM) (Amersham Biosciences).. The CodeLink Expression Bioarrays utilize nucleic acid hybridization of a biotin-labeled complementary RNA (cRNA) target with DNA oligonucleotide probes attached to a gel matrix.

The biotin-labeled cRNA target is prepared by a linear amplification method. Poly (A) + RNA (within the total RNA population) is primed for reverse transcription by a DNA oligonucleotide containing a T7 RNA polymerase promoter 5' to a (dT) 24 sequence. After second-strand cDNA synthesis, the cDNA serves as the template in an *in vitro* transcription (IVT) reaction to produce the target cRNA. The IVT is performed in the presence of biotinylated nucleotides to label the target cRNA. This procedure results in a 50-200 fold linear amplification of the input poly (A) + RNA.

Hybridization Probes.

The oligonucleotide probes were provided by the Codelink Uniset Mouse I Bioarray (Amersham, product code 300013). Amine-terminated oligonucleotide probes are attached to a three-dimensional polyacrylamide gel matrix. There are 10,000 oligonucleotide probes, each specific to a well-characterized mouse gene. Each mouse gene is representative of a unique gene cluster from the fourth quarter 2001 Genbank Unigene build. There are also 500 control probes.

The sequences of the probes are proprietary to Amersham. However, for each probe, Amersham identifies the corresponding mouse gene by NCBI accession number, OGS, LocusLink, Unigene Cluster ID, and description (name). This information should be available from Amersham. In the case of the differentially expressed probes, this information is duplicated in master table 1. For the complete list, see <http://www4.amershambiosciences.com/apatrix/upp01077.nsf/Cont>

ent/codelink_literature

Under "Gene Lists", select "Uniset Mouse I", and a gene list, in Excel format, can be downloaded.

5

Hybridization

Using the cRNA target, the hybridization reaction mixture is prepared and loaded into array chambers for bioarray processing as set forth in the manufacturer's instructions for CodeLink Gene Expression Bioarrays™ (Amersham Biosciences). Each sample is hybridized to an individual microarray. Hybridization is at 37°C. The hybridization buffer is prepared as set forth in the Motorola instructions. Hybridization to the microarray is detected with an avidinated fluorescent reagent, Streptavidin-Alexa Fluor® 647 (Amersham).

15

Mouse Gene Expression Analysis

Processed arrays were scanned using a GenePix 4000B Microarray Scanner (Axon Instruments, Inc.); array images were acquired using the Amersham CodeLink™ Analysis Software (Release 2.2). The Amersham CodeLink™ Analysis Software gives an integrated optical density (IOD) value for every spot; a unique background value for that spot is subtracted, resulting in "raw" data points. Individual chips are then normalized by the Amersham CodeLink™ software according to the median raw intensity for all 10,000 genes. A negative control threshold (0.2) is also calculated according to the control probes. The expression data was analyzed to identify genes whose expression levels changed significantly with respect to:

30

Normal mice compared to hyperinsulinemic mice at 2, 4, 8 and 16 weeks on normal vs. high-fat diet.

35

Normal mice compared to hyperinsulinemic/hyperglycemic mice at 2, 4, 8 and 16 weeks on normal vs. high-fat diet.

Hyperinsulinemic compared to hyperinsulinemic/hyperglycemic mice at 2, 4, 8 and 16 weeks on high-fat diets.

5 **Database Searches** Nucleotide sequences and predicted amino acid sequences were compared to public domain databases using the Blast 2.0 program (National Center for Biotechnology Information, National Institutes of Health). Nucleotide sequences were displayed using ABI prism Edit
10 View 1.0.1 (PE Applied Biosystems, Foster City, CA).

 Nucleotide database searches were conducted with the then current version of BLASTN 2.0.12, see Altschul, et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.*, 25:3389-3402
15 (1997). Searches employed the default parameters, unless otherwise stated.

 For blastN searches, the default was the blastN matrix (1,-3), with gap penalties of 5 for existence and 2 for extension.

20 Protein database searches were conducted with the then-current version of BLAST X, see Altschul et al. (1997), supra. Searches employed the default parameters, unless otherwise stated. The scoring matrix was BLOSUM62, with gap costs of 11 for existence and 1 for extension. The standard
25 low complexity filter was used.

 "ref" indicates that NCBI's RefSeq is the source database. The identifier that follows is a RefSeq accession number, not a GenBank accession number. "RefSeq sequences are derived from GenBank and provide non-redundant curated
30 data representing our current knowledge of known genes. Some records include additional sequence information that was never submitted to an archival database but is available in the literature. A small number of sequences are provided through collaboration; the underlying primary sequence data
35 is available in GenBank, but may not be available in any one GenBank record. RefSeq sequences are not submitted primary sequences. RefSeq records are owned by NCBI and therefore can be updated as needed to maintain current annotation or

to incorporate additional sequence information." See also <http://www.ncbi.nlm.nih.gov/LocusLink/refseq.html>

It will be appreciated by those in the art that the exact results of a database search will change from day to day, as new sequences are added. Also, if you query with a longer version of the original sequence, the results will change. The results given here were obtained at one time and no guarantee is made that the exact same hits would be obtained in a search on the filing date. However, if an alignment between a particular query sequence and a particular database sequence is discussed, that alignment should not change (if the parameters and sequences remain unchanged).

Northern Analysis.

Northern analysis may be used to confirm the results. Favorable and unfavorable genes, identified as described above, or fragments thereof, will be used as probes in Northern hybridization analyses to confirm their differential expression. Total RNA isolated from subject mice will be resolved by agarose gel electrophoresis through a 1% agarose, 1 % formaldehyde denaturing gel, transferred to positively charged nylon membrane, and hybridized to a probe labeled with [32P] dCTP that was generated from the aforementioned gene or fragment using the Random Primed DNA Labeling Kit (Roche, Palo Alto, CA), or to a probe labeled with digoxigenin (Roche Molecular Biochemicals, Indianapolis, IN), according to the manufacturer's instructions.

Real-Time RNA Analysis.

Real-time RNA analysis may also be used for confirmation. For "real-time" RNA analysis, RNA will be converted to cDNA and then probed with gene-specific primers made for each clone. "Real-time" incorporation of fluorescent dye will be measured to determine the amount of specific transcript present in each sample. Sample differences (control vs. hyperinsulinemic, hyperinsulinemic

vs. diabetic, or control vs. diabetic) will be evaluated. Confirmation using several independent animals is desirable.

In situ Hybridization

5 Another form of confirmation may be provided by nonisotopic *in situ* hybridizations (NISH) on selected human (obtained by Tissue Informatics) and mouse tissues using cRNA probes generated from mouse genes found to be up- or down-regulated during the disease progression. *In situ*
10 hybridizations may also be performed on mouse tissues using cRNA probes generated from differentially expressed DNAs. These cRNA's will hybridize to their corresponding messenger RNA's present in cells and will provide information regarding the particular cell types within a tissue that is
15 expressing the particular gene as well as the relative level of gene expression. The cRNA probes may be generated by *in vitro* transcription of template cDNA by Sp6 or T7 RNA polymerase in the presence of digoxigenin-11-UTP (Roche Molecular Biochemicals, Mannheim, Germany; Pardue, M.L.
20 1985. *In situ* hybridization, Nucleic acid hybridization, a practical approach: IRL Press, Oxford, 179-202).

Transgenic Animals.

25 Transgenic expression may be used to confirm the results. In one embodiment, a mouse is engineered to overexpress the favorable or unfavorable mouse gene in question. In another embodiment, a mouse is engineered to express the corresponding favorable or unfavorable human gene. In a
30 third embodiment, a nonhuman animal other than a mouse, such as a rat, rabbit, goat, sheep or pig, is engineered to express the favorable or unfavorable mouse or human gene.

Hyperquantitative Tissue Analysis

35 In addition to gene expression analysis the tissue sections can also be analyzed using TissueInformatics, Inc.'s TissueAnalytics™ software. A single representative section may be cut from each tissue block, placed on a slide, and stained with H&E. Digital images of each slide

may be acquired using an research microscope and digital camera (Olympus E600 microscope and Sony DKC-ST5). These images may be acquired at 20x magnification with a resolution of 0.64 mm/pixel. A hyperquantitative analysis may be performed on the resulting images: First a digital image analysis can identify and annotate structural objects in a tissue using machine vision. These objects, that are constituents of the tissue, can be annotated because they are visually identifiable and have a biological meaning like islets and tubules. Subsequently a quantification of these structures regarding their geometric properties like area or stain intensities and their relationship to the field of view or per unit area in terms of a % coverage may be performed. Features or parameters for hyper-quantification are specific for each tissue, and may also include relations between features, measures of overall heterogeneity, including orientation, relative locations, and textures.

Correlation Analysis

Mathematical statistics provides a rich set of additional tools to analyze time resolved data sets of hyper-quantitative and gene expression profiles for similarities, including rank correlation, the calculation of regression and correlation coefficients, and clustering. Continuous functions may also be fitted through the data points of individual gene and tissue feature data. Relation between gene expression and hyper-quantitative tissue data may be linear or non-linear, in synchronous or asynchronous arrangements.

Example 1

Obesity is increasing at an alarming rate in the United States. In parallel, the incidence of type II diabetes is also rising. We are interested in defining alterations in gene expression that correlate with the development of these conditions in the hopes of reversing these dangerous trends.

Insulin plays a major role in regulating blood glucose levels. It stimulates the uptake of glucose in adipose

tissue and striated muscle for storage as intracellular triglycerides and glycogen. Insulin also inhibits the release of glucose from the liver. Normally, this would prevent the rise in blood sugar concentration that occurs after eating. However, in the early stages of type 2 diabetes, resistance to insulin is seen. Initially, production and secretion of insulin from the pancreas increases to compensate for the tissue resistance. Eventually, however, the pancreas cannot keep up with the insulin resistance, blood glucose levels rise, and insulin production by the pancreas is finally exhausted.

We are utilizing a mouse model of diet-induced obesity that progresses to diabetes. The diet is high in fat, an increasing component in the U.S. diet, and has been documented to lead to diabetes in C57BL/6J mice (Surwit et al., 1988). After weaning, C57BL/6J mice were fed either the high fat diet or a standard lab chow diet for 16 weeks. Body weight was monitored bi-weekly. Fasting glucose and insulin levels were measured after 2, 4, 8, and 16 weeks on the diets.

Consumption of the HF diet resulted in significant, progressive increases in body weight and fasting insulin levels in comparison to consumption of the Std diet. Fasting glucose levels of mice on the HF diet were dramatically increased at the first time point assayed (2 weeks) and remained high through the duration of the experiment (16 weeks).

At each time point, several diabetic and control mice were sacrificed and a number of tissues collected. RNA was extracted from the pancreas at each time point.

In order to identify pancreatic genes involved in the development of type 2 diabetes, we used microarray analysis to compare RNA expression levels of 10,000 genes in pancreas of high fat diet fed and control diet fed mice at various time points in the progression of type 2 diabetes. Microarray analysis provides a more global picture of gene regulation, allowing the identification of families or groups of genes showing similar expression patterns that

potentially imply similar or coordinated roles in disease progression.

Of 10,000 genes analyzed, 115 were up-regulated and 91 down-regulated greater than two-fold in comparisons between the diabetic and non-diabetic mice. Glutathione peroxidase 1 (Gpx1, NM_008160) was one of the most down-regulated genes when comparing HF to Std mice. It decreased dramatically over the 16 week study.

Example 2

Interestingly, further analysis of the time points and exploration of gene pathways and functionally related genes revealed a subset of glutathione peroxidase, S-transferase and synthetase genes exhibiting a consistent decrease in expression in the diabetic mice; 6 of 23 glutathione peroxidase, S-transferase and synthetase genes represented on the array were decreased in diabetic pancreas at all four time points and an additional 5 were decreased at three of the four time points.

Only three of these genes had been identified using the two-fold cut-off criterion. Thus, microarray analysis combined with time point sampling can reveal subtle yet consistent changes in gene expression and identify altered metabolic pathways.

With nearly half (11 of 23) of the genes in a related family of genes being consistently down-regulated, the glutathione peroxidase, S-transferase and synthetase genes represent an interesting family for further study in pancreas expression, especially in relation to obesity and diabetes.

Introduction to Master Tables

The master tables reflect applicants' analysis of the gene chip data.

5

For each probe corresponding to a differentially expressed mouse gene, Master Table 1 identifies

Col. 1: The mouse gene (upper) and mouse protein (lower)
10 database accession #s.

Col. 2: The corresponding mouse Unigene Cluster, as of the
4th Quarter 2001 build.

15 Col. 3: The behavior (differential expression) observed for
the mouse gene. This column identifies the gene as
favorable(F) or unfavorable (U) on the basis of its
differential behavior. There are three possible
comparisons, HI-D, C-HI, and C-D, where C=control (normal),
20 HI=hyperinsulinemic, and D=diabetic. If HI>D, C>HI, or C>D,
the behavior for that subject comparison is considered
unfavorable. If the inequality is reversed, the behavior
for that subject comparison is considered favorable.

In the Master Table, the numerical value is the ratio of
25 the greater value to the lesser value. If this ratio is at
least two fold, the degree of differential expression is
considered strong. Usually only mouse genes exhibiting at
least one strong differential expression behavior are listed
in the Master Table; exceptions are noted in the Examples.

30 In some of the related applications cited above, and
perhaps occasionally in this application, a ratio may be
given as a negative number. This does not have its usual
mathematical meaning; it is merely a flag that in the
comparison, the former value was less than the latter one,
35 i.e., the gene was favorable. For the purpose of applying
the teachings of the specification concerning desired
ratios, any negative value should be converted to a positive
one by taking its absolute value.

Col. 4: A related human protein, identified by its database accession number. Usually, several such proteins are identified relative to each mouse gene. These proteins have
5 been identified by BLAST searches, as explained in cols. 6-8.

Col. 5: The name of the related human protein.

10 Col. 6: The score (in bits) for the alignment performed by the BLAST program.

Col. 7: The E-value for the alignment performed by the BLAST program. It is worth noting that Unigene considers a Blastx
15 E Value of less than $1e-6$ to be a "match" to the reference sequence of a cluster.

Unless otherwise indicated, the bit score and E-value for the alignment is with respect to the alignment of the mouse
20 DNA of col. 1 to the human protein of col. 4 by BlastX, according to the default parameters.

Master Table 1 is divided into three subtables on the basis of the behavior in col. 3. If a gene has at least one
25 significantly favorable behavior, and no significantly unfavorable ones, it is put into Subtable 1A. In the opposite case, it is put into Subtable 1B. If its behavior is mixed, i.e., at least one significantly favorable and at least one significantly unfavorable, it is put into Subtable
30 1C. Note that this classification is based on the strongest observed differential expression behaviors for each of the three subject comparisons, C-HI, HI-D and C-D.

Master Table 2 has just three columns.

35 Col. 1: Mouse gene.

Col. 2: behavior. Same as col. 3 in Master table 1.

Col. 3: Human protein classes. Based on the related human proteins defined in Master Table 1, Master Table 2 generalizes, if possible as to classes of human proteins which are expected to have similar behavior. For a given mouse gene, several human protein classes may be listed because of the diversity of the human proteins found to be related. In some cases, the stated human protein classes may be hierarchical, e.g., one may be a subset of another. In other cases, the stated classes may be non-overlapping but related. And in yet other cases, the stated classes may be non-overlapping and unrelated. Combinations of the above are also possible.

In addition to the classes stated, the corresponding human gene clusters are also of interest. These may be obtained in a number of ways. First, one may search on Unigene (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene>) for the identified human protein. Review the "hits" (each of which is a Unigene record) for those prefixed by "Hs." Secondly, one may access the Unigene record for the mouse gene cluster (which is given in Master Table 1), and then click on "Homologene". This will bring up a new page which includes the section "Possible Homologous Genes". One of the entries should be a Homo sapiens gene (considered by Unigene to be the most related human gene); click on its Unigene record link.

Additional information of interest may be accessed by searching with the mouse gene accession # in the Mouse Gene Informatics database, at <http://www.informatics.jax.org/>.

MASTER TABLE 1: SIGNIFICANTLY DIFFERENTIALLY EXPRESSED MOUSE GENES/PROTEINS AND CORRESPONDING HUMAN GENES/PROTEINS

Subtable 1A: Favorable Mouse Genes/Proteins and Corresponding Human Genes/Proteins

Mouse Gene/Protein	Mouse Gene/Protein	Mouse Gene/Protein	Human Gene/Protein	Human Gene/Protein	Human Gene/Protein
Genes/Proteins selected as described in Example 2. First three mouse genes also qualify by criteria of Example 1.					
NM_008180	F:(G-D)+	NP_000169.1	glutathione synthetase; GSH synthetase; glutathione synthase	810	0
NP_032206.1	2.60				
NM_010344	F:(G-D)+	NP_000628.1	glutathione synthetase; GSH synthetase; glutathione synthase	792	0
NP_034474.3	2.31				
		4GR1	Glutathione Synthetase (E.C.1.6.4.2) Oxidized Form Complexed With Retro-Gssg	789	0
		1GR1	Human Glutathione Synthetase A34eR37W MUTANT	788	0
		1DNC	Human Glutathione Synthetase Modified By Dinitrosoglutathione	787	0
		1XAN	Human Glutathione Synthetase In Complex With A Xanthine Inhibitor	784	0
		2GR1	Human Glutathione Synthetase A34e, R37w Mutant, Oxidized Glutathione Complex	782	0
		1K4Q_A	Chain A, Human Glutathione Synthetase Inactivated By Peroxynitrite	781	0
		1GSN	Human Glutathione Synthetase Modified By Dinitrosoglutathione	773	0
		CAA38387.1	glutathione synthetase	771	0
		TXN2_HUMAN	Thioredoxin reductase 2, mitochondrial precursor (TR2) (TR-beta)	335	2e-81
		AAD19597.1	thioredoxin reductase	268	5e-71
		NP_006431.2	thioredoxin reductase 2 isoform 1 precursor; thioredoxin reductase 3; selenoprotein Z; thioredoxin reductase beta	268	5e-71
				268	5e-71

			NP_665691.1	thioredoxin reductase 2 isoform 3; thioredoxin reductase 3; selenoprotein Z;	268	5e-71
			AAD25167.1	thioredoxin reductase beta	268	5e-71
			AAG47635.1	thioredoxin reductase	268	5e-71
			BAA77601.2	mitochondrial thioredoxin reductase	266	1e-70
			BAA77602.2	thioredoxin reductase II alpha	266	1e-70
			AAC69621.1	thioredoxin reductase II beta	239	1e-62
			BAA13674.1	thioredoxin reductase GRIM-12	239	2e-62
			AAF15900.1	KM-102-derived reductase-like factor	239	2e-62
			CAA04503.1	thioredoxin reductase	239	2e-62
			NP_877393.1	thioredoxin reductase	239	2e-62
			AAL15432.1	thioredoxin reductase 1; KM-102-derived reductase-like factor; thioredoxin reductase GRIM-12	238	3e-62
			TXN1_HUMAN	thioredoxin reductase 1	238	3e-62
			S66877	thioredoxin reductase, cytoplasmic precursor (TR) (TR1)	238	3e-62
			NP_665690.1	thioredoxin-disulfide reductase (EC 1.8.1.9) [validated] - human	238	3e-62
			BAC87474.1	thioredoxin reductase 2 isoform 2; thioredoxin reductase 3; selenoprotein Z;	237	9e-62
			AAD51325.1	thioredoxin reductase beta	236	1e-61
			AAH50032.1	unnamed protein product	236	2e-61
			AAF21432.1	thioredoxin reductase TR2	236	2e-61
			XP_051264.5	TXNRD3 protein	236	2e-61
			AAH30028.1	selenoprotein Zf2	236	2e-61
			AAD39925.1	thioredoxin reductase 3	235	3e-61
			NP_057001.1	thioredoxin reductase 3	235	3e-61
			F:(C-D)+ 2.01	thioredoxin reductase 3	346	3e-95
AK002661	Mm.267014		NP_057001.1	glutathione transferase kappa 1; glutathione S-transferase subunit13 homolog	345	6e-95
BAB22268.1			AAP97160.1	GSTK1-1	345	6e-95

			AAF65506.1	HDCMD47P		340	2e-93
			AAH63425.1	GSTK1 protein		276	3e-74
NIM_010356		F/(C-D)+					
NP_034486.2	Mm.14719	1.73	AAAT4634.1	glutathione S-transferase A3		353	3e-97
				glutathione S-transferase A3; glutathione S-alkyltransferase A3; glutathione S-aryltransferase A3; S-(hydroxyalkyl)glutathione lyase A3; glutathione S-alkyltransferase A3; glutathione transferase, alpha 3; glutathione S-transferase A3-3; GST class-alpha			
			NP_000838.3			352	7e-97
			AAH20619.1	Glutathione S-transferase A3		350	2e-96
			A49365	glutathione transferase (EC 2.5.1.18) alpha-3		350	3e-96
				glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1; glutathione S-alkyltransferase A1; GST-epsilon; glutathione S-transferase 2		338	9e-93
			NP_665683.1			336	3e-92
			1GUH_A	Chain A, Glutathione S-Transferase A1-1 (EC 2.5.1.18)		336	3e-92
			1GUH_B	Chain B, Glutathione S-Transferase A1-1 (EC 2.5.1.18)		335	7e-92
			1GSE_A	Chain A, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R15K)		335	7e-92
			1GSE_B	Chain B, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R15K)		333	3e-91
			AA436174.1	glutathione S-transferase subunit 1 (GST, EC 2.5.1.18)		332	6e-91
			AAB23672.1	glutathione S-transferase A2 subunit		331	1e-90
			SZ4330	glutathione transferase (EC 2.5.1.18) alpha-2			
				glutathione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-alkyltransferase A2; GST-gamma; HA subunit 2		330	2e-90
			NP_000837.2	dJ162L7.3 (glutathione S-transferase A2)		330	2e-90
			CAB92770.1			323	2e-88
			CAA46643.1	glutathione S-transferase			
			NP_714543.1	glutathione transferase A5		320	3e-87

					glutathione transferase			296	5e-80
					glutathione transferase (EC 2.5.1.18) omega-1 chain			277	2e-74
					glutathione transferase (EC 2.5.1.18) omega-2 chain			272	8e-73
					alpha-class glutathione S-transferase omega 1 subunit [human, liver, Peptide Partial, 169 aa, segment 1 of 3]			270	3e-72
					alpha-class glutathione S-transferase omega 2 subunit [human, liver, Peptide Partial, 169 aa, segment 1 of 3]			265	1e-70
					glutathione S-transferase A4; glutathione S-alkyltransferase A4; glutathione S-aryltransferase A4; (hydroxyalkyl)glutathione lyase A4; glutathione S-alkyltransferase A4; glutathione transferase A4-4; class-alpha; glutathione S-transferase, alpha 4			242	6e-64
NM_008184 NP_032210.1					glutathione transferase M1			342	4e-94
					glutathione S-transferase M1 isoform 1; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1			341	5e-94
					Chain A, Ligand-Free Human Glutathione S-Transferase M1a-1a			339	2e-93
					Chain B, Ligand-Free Human Glutathione S-Transferase M1a-1a			339	2e-93
					Chain C, Ligand-Free Human Glutathione S-Transferase M1a-1a			339	2e-93
					Chain D, Ligand-Free Human Glutathione S-Transferase M1a-1a			339	2e-93
					glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2			334	8e-92
					Chain A, Ligand-Free Human Glutathione S-Transferase M2-2(E.C.2.5.1.18), Monoclinic Crystal Form			332	3e-91
					Chain B, Ligand-Free Human Glutathione S-Transferase M2-2(E.C.2.5.1.18), Monoclinic Crystal Form			332	3e-91

			3GTUA	Chain A, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Formse	332	3e-91
			3GTUC	Chain C, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18)	332	3e-91
			1HNA	Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (Ec 2.5.1.18) Mutant With Trp 214 Replaced By Phe(W214f)	328	4e-90
			1HNAA	Chain A, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form B (Ec 2.5.1.18) Mutant With Trp 214 Replaced By Phe(W214f)	328	4e-90
			1HNBB	Chain B, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form B (Ec 2.5.1.18) Mutant With Trp 214 Replaced By Phe(W214f)	328	4e-90
			1HNCA	Chain A, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (Ec 2.5.1.18) Mutant With Trp 214 Replaced By Phe(W214f)	328	4e-90
			1HNCB	Chain B, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (Ec 2.5.1.18) Mutant With Trp 214 Replaced By Phe(W214f)	328	4e-90
			1HNCC	Chain C, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (Ec 2.5.1.18) Mutant With Trp 214 Replaced By Phe(W214f)	328	4e-90
			1HNCD	Chain D, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (Ec 2.5.1.18) Mutant With Trp 214 Replaced By Phe(W214f)	328	4e-90
				glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyaseM4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4		
			NP_000841.1		326	2e-89
			P46439	Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)	325	3e-89
			AAA57346.1	glutathione transferase M4	325	4e-89
			S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4	325	4e-89
			4GTUA	Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (Ec 2.5.1.18)	325	5e-89
			4GTUB	Chain B, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (Ec 2.5.1.18)	325	5e-89

			4GTUC	Chain C, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	325	5e-89
			4GTUD	Chain D, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	325	5e-89
			4GTUE	Chain E, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	325	5e-89
			4GTUF	Chain F, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	325	5e-89
			4GTUG	Chain G, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	325	5e-89
			4GTUH	Chain H, Ligand-Free Homodimeric Human Glutathione S-Transferase	325	5e-89
			AAH58881.1	Glutathione S-transferase M5	324	6e-89
				glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5	324	
			NP_000842.2	glutathione S-transferase	324	6e-89
			CAA48638.1	Chain B, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	286	2e-80
			3GTUB	Chain D, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	288	4e-78
			3GTUD	glutathione S-transferase M3; glutathione S-transferase, Mu-3; brain GST; glutathione S-alkyltransferase M3; glutathione S-aryltransferase M3; S-(hydroxyalkyl)glutathione lyase M3; glutathione S-alkyltransferase M3; GST class-mu 3	288	4e-78
			NP_000840.2	Glutathione S-transferase M3	288	4e-78
			AAH08780.1	glutathione transferase (EC 2.5.1.18) class mu, GSTM3	288	4e-78
			A35295	glutathione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	285	3e-77
			NP_671489.1		283	2e-76

				NP_086533.1	glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-aryltransferase; GST class-mu 1	256	2e-68
				BAC86900.1	unnamed protein product	213	2e-55
NM_008182					glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; glutathione S-alkyltransferase A1; GST-epsilon; glutathione S-transferase 2	328	9e-90
NP_032206.1	Mm.197422	F:(C-D)+ 1.51		NP_085683.1	glutathione S-transferase subunit 1 (GST, EC 2.5.1.18)	327	1e-89
				AAA36174.1	glutathione S-transferase A5	327	1e-89
				NP_714543.1	glutathione transferase A5	326	3e-89
				1GUH_A	Chain A, Glutathione S-Transferase A1-1 (EC 2.5.1.18)	326	3e-89
				1GUH_B	Chain B, Glutathione S-Transferase A1-1 (EC 2.5.1.18)	326	3e-89
				1GSF_A	Chain A, Glutathione Transferase A1-1 Complexed With Ethacrynic Acid	326	3e-89
				1GSF_B	Chain B, Glutathione Transferase A1-1 Complexed With Ethacrynic Acid	326	3e-89
				1GSD_A	Chain A, Glutathione Transferase A1-1 In Unliganded Form	326	3e-89
				1GSD_B	Chain B, Glutathione Transferase A1-1 In Unliganded Form	326	3e-89
				1K3L_A	Chain A, Crystal Structure Analysis Of S-Hexyl-Glutathione Complex Of Glutathione Transferase At 1.5 Angstroms Resolution	326	3e-89
				1K3L_B	Chain B, Crystal Structure Analysis Of S-Hexyl-Glutathione Complex Of Glutathione Transferase At 1.5 Angstroms Resolution	326	3e-89
				1K3O_A	Chain A, Crystal Structure Analysis Of Apo Glutathione S-Transferase	326	3e-89
				1K3O_B	Chain B, Crystal Structure Analysis Of Apo Glutathione S-Transferase	326	3e-89
				1K3Y_A	Chain A, Crystal Structure Analysis Of Human Glutathione S-Transferase With S-Hexyl Glutathione And Glycerol At 1.3 Angstrom	326	3e-89
				1K3Y_B	Chain B, Crystal Structure Analysis Of Human Glutathione S-Transferase With S-Hexyl Glutathione And Glycerol At 1.3 Angstrom	326	3e-89
				1GSE_A	Chain A, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant/R15k)	325	8e-89

		1GSE_B	Chain B, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R16K)	325	8e-89
			glutathione S-transferase A3; glutathione S-alkyltransferase A3; glutathione S-aryltransferase A3; S-(hydroxyalkyl)glutathione lyase A3; glutathione S-alkyltransferase A2; glutathione transferase, alpha 3; glutathione S-transferase A3-3; GST class-alpha	324	1e-88
		NP_000838.3	Glutathione S-transferase A3	322	4e-88
		AAH20819.1	glutathione transferase (EC 2.5.1.18) alpha-3 [similarity] - human	322	5e-88
		A49365	glutathione S-transferase A3	322	5e-88
		AAH74634.1	glutathione S-transferase A2 subunit	317	1e-86
		AA523672.1	glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2) - human	316	3e-86
		S24330	glutathione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-alkyltransferase A2; GST-gamma; HA subunit 2		
		NP_000837.2	dJ152L7.3 (glutathione S-transferase A2)	315	5e-86
		CAB92770.1	glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2 (+)) - human	315	5e-86
		S77988	glutathione transferase	309	3e-84
		AAD04712.1	glutathione transferase	272	4e-73
		S29657	glutathione transferase (EC 2.5.1.18) omega-1 chain - human (fragments)	262	5e-70
		S29658	glutathione transferase (EC 2.5.1.18) omega-2 chain - human (fragments)	253	3e-67
		AA525364.1	alpha-class glutathione S-transferase omega 1 subunit [human, liver, Peptide Partial, 169 aa, segment 1 of 3]	252	5e-67
		AA525369.1	alpha-class glutathione S-transferase omega 2 subunit [human, liver, Peptide Partial, 169 aa, segment 1 of 3]	243	3e-64
			glutathione S-transferase A4; glutathione S-alkyltransferase A4; glutathione S-aryltransferase A4; S-(hydroxyalkyl)glutathione lyase A4; glutathione S-alkyltransferase A4; glutathione transferase A4-4; GST class-alpha; glutathione S-transferase, alpha 4		
		NP_001503.1	Chain A, Human Glutathione Transferase A4-4 Complex With Iodobenzyl Glutathione	221	2e-57
		1GUL_A		221	2e-57

				1GUL_B	Chain B, Human Glutathione Transferase A4-4 Complex With Iodobenzyl Glutathione	221	2e-57
				1GUL_C	Chain C, Human Glutathione Transferase A4-4 Complex With Iodobenzyl Glutathione	221	2e-57
				1GUL_D	Chain D, Human Glutathione Transferase A4-4 Complex With Iodobenzyl Glutathione	221	2e-57
				1GUL_E	Chain E, Human Glutathione Transferase A4-4 Complex With Iodobenzyl Glutathione	221	2e-57
				1GUL_F	Chain F, Human Glutathione Transferase A4-4 Complex With Iodobenzyl Glutathione	221	2e-57
				1GUL_G	Chain G, Human Glutathione Transferase A4-4 Complex With Iodobenzyl Glutathione	221	2e-57
				1GUL_H	Chain H, Human Glutathione Transferase A4-4 Complex With Iodobenzyl Glutathione	221	2e-57
NM_010360 NP_034490.1	Mm.282351	F(C-D)+ 1.40		3GTUB	Chain B, Ligand-Free Heterodimeric Human Glutathione S-TransferaseM2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	419	e-117
				3GTUD	Chain D, Ligand-Free Heterodimeric Human Glutathione S-TransferaseM2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	419	e-117
				NP_000840.2	glutathione S-transferase M3; glutathione S-transferase, Mu-3; brain GST; glutathione S-alkyltransferase M3; glutathione S-aryltransferase M3; S-(hydroxyalkyl)glutathione lyase M3; glutathione S-alkyltransferase M3; GST class-mu 3- ³	419	e-117
				AAH08790.1	Glutathione S-transferase M3	419	e-117
				A35295	glutathione transferase (EC 2.5.1.18) class mu, GSTM3	416	e-116
					glutathione S-transferase M1 isoform 1; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1	332	4e-91
				NP_000552.2	Chain A, Ligand-Free Human Glutathione S-Transferase M1a-1a	332	4e-91
				1GTUA	Chain B, Ligand-Free Human Glutathione S-Transferase M1a-1a	332	4e-91
				1GTUB	Chain B, Ligand-Free Human Glutathione S-Transferase M1a-1a	332	4e-91

		1GTUC	Chain C, Ligand-Free Human Glutathione S-Transferase M1a-1a	332	4e-91
		1GTUD	Chain D, Ligand-Free Human Glutathione S-Transferase M1a-1a	332	4e-91
		AAA59203.1	glutathione transferase M1	330	2e-90
		S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4	326	3e-89
			glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase M4; GTS-Mu2; GST, class-mu 4	325	6e-89
		NP_000841.1	Chain A, Ligand-Free Homodimeric Human Glutathione S- M4- 4 (E.C.2.5.1.18)	325	6e-89
		4GTUA	Chain B, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	325	6e-89
		4GTUB	Chain C, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	325	6e-89
		4GTUC	Chain D, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	325	6e-89
		4GTUD	Chain E, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	325	6e-89
		4GTUE	Chain F, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	325	6e-89
		4GTUF	Chain G, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	325	6e-89
		4GTUG	Chain H, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	325	6e-89
		4GTUH	Chain I, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	325	6e-89
		AAA57346.1	glutathione transferase M4	324	1e-88
			glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2	322	5e-88
		NP_000839.1	Chain A, Ligand-Free Human Glutathione S-Transferase M2-2 (E.C.2.5.1.18), Monoclinic Crystal Form	322	5e-88
		2GTUA		322	5e-88

		2GTUB	Chain B, Ligand-Free Human Glutathione S-Transferase M2-2 (E.C.2.5.1.18), Monoclinic Crystal Form	322	5e-88
		3GTUA	Chain A, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (E.C.2.5.1.18), Monoclinic Crystal Form	322	5e-88
		3GTUC	Chain C, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (E.C.2.5.1.18), Monoclinic Crystal Form	322	5e-88
		AAH58881.1	Glutathione S-transferase M5	320	2e-87
		NP_000842.2	glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5	320	2e-87
		P46439	Glutathione S-transferase Mu 5 (GSTM5-5)	320	2e-87
		1HNA	Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	318	8e-87
		1HNBA	Chain A, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form B (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	318	8e-87
		1HNBB	Chain B, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form B (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	318	8e-87
		1HNCA	Chain A, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	318	8e-87
		1HNGB	Chain B, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	318	8e-87
		1HNCC	Chain C, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	318	8e-87
		1HNCD	Chain D, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	318	8e-87
		CAA48636.1	glutathione S-transferase	295	9e-80
			S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	293	2e-79

J03953 NP_034489			NP_666533.1 BAC86900.1	glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1 unnamed protein product	253	2e-67
			BAC86900.1		202	8e-52
J03953 NP_034489	Mm.347436	F:(C-D)+ 1.40	1GTUJA	Chain A, Ligand-Free Human Glutathione S-Transferase M1a-1a	352	5e-97
			1GTUJB	Chain B, Ligand-Free Human Glutathione S-Transferase M1a-1a	352	5e-97
			1GTUJC	Chain C, Ligand-Free Human Glutathione S-Transferase M1a-1a	352	5e-97
			1GTUJD	Chain D, Ligand-Free Human Glutathione S-Transferase M1a-1a	352	5e-97
				glutathione S-transferase M1 isoform 1; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1	352	5e-97
			NP_000552.2	glutathione transferase M1	350	2e-96
			AAA5203.1	Chain A, Ligand-Free Human Glutathione S-Transferase M2-2 (E.C.2.5.1.18), Monoclinic Crystal Form	348	1e-95
			2GTU_A	Chain B, Ligand-Free Human Glutathione S-Transferase M2-2 (E.C.2.5.1.18), Monoclinic Crystal Form	348	1e-95
			2GTU_B	Chain C, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (E.C.2.5.1.18), Monoclinic Crystal Form	348	1e-95
			3GTU_A	Chain C, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (E.C.2.5.1.18), Monoclinic Crystal Form	348	1e-95
			3GTU_C	glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2	348	1e-95
			NP_000839.1	Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214F)	344	2e-94
			1HNA	Chain A, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form B (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214F)	344	2e-94

		1HNB_B	Chain B, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form B (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	344	2e-94
		1HNC_A	Chain A, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	344	2e-94
		1HNC_B	Chain B, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	344	2e-94
		1HNC_C	Chain C, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	344	2e-94
		1HNC_D	Chain D, Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form C (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	344	2e-94
		4GTU_A	Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	342	8e-94
		4GTU_B	Chain B, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	342	8e-94
		4GTU_C	Chain C, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	342	8e-94
		4GTU_D	Chain D, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	342	8e-94
		4GTU_E	Chain E, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	342	8e-94
		4GTU_F	Chain F, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	342	8e-94
		4GTU_G	Chain G, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	342	8e-94
		4GTU_H	Chain H, Ligand-Free Homodimeric Human Glutathione S-Transferase M4-4 (E.C.2.5.1.18)	342	8e-94
			glutathione S-transferase M4 isoform 1; glutathione S-transferase, MU-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-hydroxyalkylglutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	342	8e-94
		NP_000841.1	glutathione transferase M4	340	2e-93

			S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4 (version 2) - human	338	9e-93
			GTM5_HUMAN	Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)	337	2e-92
			AAH58881.1	Glutathione S-transferase M5	336	4e-92
				glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5		
			NP_000842.2		336	4e-92
			CAA48636.1	glutathione S-transferase	302	7e-92
			3GTU_B	Chain B, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	297	2e-80
			3GTU_D	Chain D, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	297	2e-80
			NP_000840.2	glutathione S-transferase M3; glutathione S-transferase, Mu-3; brain GST; glutathione S-alkyltransferase M3; glutathione S-aryltransferase M3; S-(hydroxyalkyl)glutathione lyase M3; glutathione S-alkyltransferase M3; GST class-mu 3		
			AAH08780.1	Glutathione S-transferase M3	297	2e-80
				glutathione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	296	3e-80
			NP_671489.1		294	2e-79
			A35295	glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human		
				glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1	270	2e-72
			NP_666533.1		270	2e-72
			AAH24005.1	Glutathione S-transferase M1, isoform 2	219	6e-57
			BAC86900.1	unnamed protein product		
NM_010363 NP_034493.1			F:(C-D)+ 1.20	glutathione transferase zeta 1	370	e-102

			1FW1_A	Chain A, Glutathione Transferase Zeta1(MALEYLACETOACETATE ISOMERASE)	388	e-101
				glutathione transferase zeta 1 isoform 1; glutathione s-transferase Zeta 1; maleylacetone isomerase; glutathione S-alkyltransferase; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; maleylacetate isomerase	367	e-101
			NP_665877.1	MAAI_HUMAN	365	e-100
				Maleylacetate isomerase (MAAI) (Glutathione S-transferase zeta 1) (GSTZ1-1)		
				glutathione transferase zeta 1 isoform 2; glutathione s-transferase Zeta 1; maleylacetone isomerase; glutathione S-alkyltransferase; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; maleylacetate isomerase	277	4e-74
			NP_665878.1			
				glutathione transferase zeta 1 isoform 3; glutathione s-transferase Zeta 1; maleylacetone isomerase; glutathione S-alkyltransferase; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; maleylacetate isomerase	265	2e-70
			NP_001504.2	Glutathione S-transferase theta ¹ (GST class-theta) (Glutathione transferase T1-1)	396	e-110
NM_008185			GTT1_HUMAN	glutathione S-transferase theta 1	393	e-109
NP_032211.2	Mm.2746	F:(C-D)+ 1.14	AAH07065.1	Glutathione S-transferase theta 1	393	e-109
			NP_000845.1	glutathione S-transferase theta 2	228	1e-59
			1LJR_A	Chain A, Glutathione Transferase (Hgst T2-2) From Human	228	1e-59
			1LJR_B	Chain B, Glutathione Transferase (Hgst T2-2) From Human	228	1e-59
			2LJR_A	Chain A, Glutathione Transferase Apo-Form From Human	228	1e-59
			2LJR_B	Chain B, Glutathione Transferase Apo-Form From Human	228	1e-59
			3LJR_A	Chain A, Glutathione Transferase (Theta Class) From Human In Complex With The Glutathione Conjugate Of 1-Menaphthyl Sulfate	228	1e-59
			3LJR_B	Chain B, Glutathione Transferase (Theta Class) From Human In Complex With The Glutathione Conjugate Of 1-Menaphthyl Sulfate	228	1e-59
			AAB63956.1	glutathione S-transferase theta 2	228	1e-59

			AAH02415.1	Glutathione S-transferase theta 2	228	1e-59
			CAG30396.1	GSTT2	228	1e-59
			AAG02373.1	glutathione S-transferase theta 2	228	1e-59
			CAG33210.1	GSTT2	228	1e-59
			AAC13317.1	glutathione S-transferase theta 2	219	8e-57
			CAG30260.1	Em-AP000351.3	203	4e-52
			CAG30385.1	GSTT1	197	2e-50
Genes/Proteins Selected as Described in Example 1						
NM_017370						
NP_059066.1	Mm.26730	F:(H-D) +6.61°	CAA25928.1	haptoglobin	599	e-171
			P00737	Haptoglobin-1 precursor	598	e-171
			HPHU1	haptoglobin precursor, allele 1 [validated]	598	e-171
			AAAS2684.1	preprohaptoglobin	598	e-171
			CAA25267.1	haptoglobin alpha 1S	598	e-171
			AAC27432.1	haptoglobin ³	597	e-170
			NP_068275.2	haptoglobin-related protein; Haptoglobin-related locus	569	e-162
			P00739	Haptoglobin-related protein precursor	569	e-162
			HPHUR	haptoglobin-related protein precursor	569	e-162
			AAAS8079.1	haptoglobin-related protein	569	e-162
			AAAS8081.1	haptoglobin-related protein	569	e-162
			CAA25927.1	haptoglobin	568	e-162
			CAA61501.1	haptoglobin-related protein	565	e-161
			AAC27433.1	haptoglobin-related protein precursor	565	e-161
			AAAS2687.1	haptoglobin precursor	559	e-159
			NP_005134.1	haptoglobin	559	e-159
			P00738	Haptoglobin-2 precursor	559	e-159
			HPHU2	haptoglobin precursor, allele 2	559	e-159

			CAA25137.1	haptoglobin precursor	559 e-159
			AA488078.1	haptoglobin	559 e-159
			AAA88080.1	haptoglobin	559 e-159
			AAA52885.1	preprohaptoglobin	559 e-159
			1006264A	haptoglobin Hp2	508 e-144
AK003138		F:(H1-D)		adipose most abundant gene transcript 1; adiponectin	419 e-117
BAB22597.1	Mm.3969	+5.96	NP_004788.1	Adiponectin precursor (30 kDa adipocyte complement-related protein) (ACRP30) (Adipose most abundant gene transcript 1) (apM1-1) (Gelatin-binding protein)	
			Q15848	gelatin-binding 28K protein precursor	419 e-117
			JC4708	a novel adipose specific collagen-like factor, apM1 a novel adipose specific collagen-like factor; apM1 abundant gene transcript 1) [Homo sapiens]	419 e-117
			BAA08227.1	adipocyte-specific secretory protein	419 e-117
			CAB52413.1	gelatin-binding protein	419 e-117
			BAA88716.1	Carbonic anhydrase III (Carbonate dehydratase III) (CA-III)	510 e-144
NM_007606		F:(H1-D)		carbonic anhydrase III, muscle specific	510 e-144
NP_031632.1	Mm.300	+5.52	P07451	carbonic anhydrase III	510 e-144
			AAH04897.1	carbonate dehydratase (EC 4.2.1.1) III	510 e-144
			NP_005172.1	carbonic anhydrase III	510 e-144
			CRH03	carbonic anhydrase III	510 e-144
			AA452293.1	anhydrase, carbonic	508 e-144
			1205233A	Carbonic Anhydrase II (Carbonate Dehydratase)(Hca II) (E.C.4.2.1.1) Mutant With Leu 198 Replaced By Phe (L198f) Complexed With Transition State Analog Acetazolamide	332 5e-91
			1YDB	Carbonic Anhydrase II (Carbonate Dehydratase)(Hca II) (E.C.4.2.1.1) Mutant With Leu 198 Replaced By Phe (L198f)	332 5e-91
			1YDC	Chain A, Site-Specific Mutant (His64 Replaced With Ala) Of Human Carbonic Anhydrase II Complexed With 4-Methylimidazole	332 7e-91
			1GOE		

			1G0F	Chain A, Site-Specific Mutant (His64 Replaced With Ala) Of Human Carbonic Anhydrase II	332	7e-91
			1MOO	Chain A, Site Specific Mutant (H64a) Of Human Carbonic Anhydrase II At High Resolution	332	7e-91
			NP_000058.1	carbonic anhydrase II; carbonic anhydrase II; carbonic dehydratase; carbonic anhydrase B [Homo sapiens]	332	7e-91
			P00918	Carbonic anhydrase II (Carbonate dehydratase II) (CA-II) (Carbonic anhydrase C)	332	7e-91
			CRH2	carbonate dehydratase (EC 4.2.1.1) II [validated]	332	7e-91
			1CA3	Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II)[E.C.4.2.1.1] (pH 5.7)	332	7e-91
			1HCA	Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II)[E.C.4.2.1.1] (pH 6.5)	332	7e-91
			4CA2	Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II)[E.C.4.2.1.1]	332	7e-91
			1CNY	Mol. Id: 1; Molecule: Carbonic Anhydrase II; Chain: Null; Synonym:Carbonate Dehydratase, Hca II; Ec: 4.2.1.1; Heterogen:Amidocarbonylbenzenesulfonamide	332	7e-91
			1CNX	Mol. Id: 1; Molecule: Carbonic Anhydrase II; Chain: Null; Synonym:Carbonate Dehydratase, Hca II; Ec: 4.2.1.1; Heterogen:Benzenesulfonamide	332	7e-91
			1CNW	Mol. Id: 1; Molecule: Carbonic Anhydrase II; Chain: Null; Synonym:Carbonate Dehydratase, Hca II; Ec: 4.2.1.1; Heterogen:Ethylamidocarbonylbenzenesulfonamide	332	7e-91
			1EOU	A Chain A, Crystal Structure Of Human Carbonic Anhydrase II Complexed With An Anticonvulsant Sugar Sulfamate	332	7e-91
			1KWQ	A Chain A, Human Carbonic Anhydrase II Complexed With Inhibitor2000-07	332	7e-91
			1KWR	A Chain A, Human Carbonic Anhydrase II Complexed With Inhibitor0134-36	332	7e-91
			CAA68426.1	carbonic anhydrase II (AA 1-265)	332	7e-91
			AAA51908.1	carbonic anhydrase II	332	7e-91
			AAA51909.1	carbonic anhydrase II	332	7e-91
			AAA51911.1	carbonic anhydrase II	332	7e-91
			1UGF	Human Carbonic Anhydrase II [hcal] (E.C.4.2.1.1) Mutant With Ala 65 Replaced By Thr (A65)	332	7e-91

			1HEC	Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II)(E.C.4.2.1.1) Mutant With Leu 198 Replaced By His(L198H)	331	9e-91
			1HED	Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II)(E.C.4.2.1.1) Mutant With Leu 198 Replaced By Ala(L198A)	331	1e-90
			1HEA	Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II)(E.C.4.2.1.1) Mutant With Leu 198 Replaced By Arg(L198R)	330	2e-90
NM_025404 NP_079680.1	Mm.5376	F:(H-D) +4.15	AAH00043.1	ADP-ribosylation factor 4-like	359	5e-99
			BA991080.1	ADP-ribosylation factor 4L	359	5e-99
			NP_001652.1	ADP-ribosylation factor 4-like; ADP-ribosylation factor-like 6	357	2e-98
			P49703	ARLL_HUMAN:ADP-ribosylation factor-like protein 4L	357	2e-98
			A57646	ADP-ribosylation factor 4-like	357	2e-98
			AA457128.1	ADP-ribosylation factor	357	2e-98
			AAA93229.1	ADP-ribosylation factor	348	1e-95
			NP_005729.1	ADP-ribosylation factor-like 4	233	3e-61
			P40617	ARL4_HUMAN ADP-ribosylation factor-like protein 4	233	3e-61
			AAB39713.1	ADP-ribosylation factor-like protein 4	233	3e-61
			AAH01111.1	ADP-ribosylation factor-like 4	233	3e-61
			AAH03027.1	ADP-ribosylation factor-like 4	233	3e-61
			AAH12804.1	AF493890_1 ADP-ribosylation factor-like protein 4	233	3e-61
			NP_005728.2	ADP-ribosylation factor-like 7	222	8e-58
			P66559	ARL7_HUMAN ADP-ribosylation factor-like protein 7 (ADP-ribosylation	222	8e-58
			CAB44355.1	ADP-ribosylation factor-like protein 7	222	8e-58
			AAH12806.1	AF493892_1 ADP-ribosylation factor-like protein 7	222	8e-58
			BA475473.1	ADP ribosylation factor-like protein	209	9e-54
			AAH01051.1	ADP-ribosylation factor-like 7	209	9e-54
NM_008042 NP_032068.1	Mm.3522	F:(H-D) +2.98	AAA58481.1	FMLP-related receptor II	491	e-139

			NP_001453.1	formyl peptide receptor-like 1; lipoxin A4 receptor (formyl peptide receptor related)	491 e-138
			P25090	FML1_HUMAN FMLP-related receptor I (FMLP-R-I) (Lipoxin A4 receptor) (LXA4 receptor) (RFP) (HM63)	491 e-138
			B42009	FMLP-related receptor 1	491 e-138
			CAA45319.1	Lipoxin A4 receptor	491 e-138
			AAA52473.1	formyl peptide receptor	491 e-138
			AAA60070.1	formyl peptide receptor	491 e-138
			BAA01720.1	FMLP-related receptor	491 e-138
			AAB23104.1	RFP=formyl peptide receptor homolog [human, bone marrow, Peptide, 351 aa]	491 e-138
			AAB51133.1	lipoxin A4 receptor	491 e-138
			AAC13684.1	lipoxin A4 receptor	491 e-138
			AAF87844.1	AC018755_3 formyl peptide receptor-like 1	491 e-138
			AAH29125.1	formyl peptide receptor-like 1	491 e-138
			AAA52474.1	N-formyl peptide receptor-like 2 protein	422 e-118
			AAC72102.1	FML2_HUMAN	422 e-118
			NP_002021.2	formyl peptide receptor-like 2	419 e-117
			P25089	FML2_HUMAN FMLP-related receptor II	419 e-117
			C42009	FMLP-related receptor 2	419 e-117
			AAA58482.1	FMLP-related receptor 1	419 e-117
			NP_002020.1	formyl peptide receptor 1	402 e-112
			AAA35847.1	N-formylpeptide receptor FMLP-R26	402 e-112
			AAF87842.1	AC018755_1 formyl peptide receptor 1; FPR1	402 e-112
			AAH05315.1	formyl peptide receptor 1	402 e-112
			P21462	FMLR_HUMAN Met-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor) (FPR) (N-formylpeptide chemoattractant receptor)	399 e-111
			AAA35846.1	N-formylpeptide receptor FMLP-R98	399 e-111

			A42009	N-formyl peptide receptor	398	e-110
			AAA16863.1	N-formyl peptide receptor	398	e-110
			AAA36362.1	N-formylpeptide receptor MLP-R98	396	e-110
			AAC51258.1	orphan G-protein coupled receptor Dez isoform a	210	3e-54
			Q95788	CvML1_HUMAN Chemokine receptor-like 1 (G-protein coupled receptor DEZ) (G protein-coupled receptor ChemR23)	207	2e-53
AK006553		F:(H-D)	NP_695550.1	hypothetical protein FLJ32702	397	e-110
BAB24650.1	Mm.59283	+2.89	BAB71401.1	unnamed protein product	397	e-110
AK003182		F:(H-D)	NP_524144.1	fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2 catalytic	301	1e-81
BAB22625.1	Mm.1000	+2.76	P06976	MLE1_HUMAN Myosin light chain 1, skeletal muscle isoform (MLC1F)	301	1e-81
			MOHUA1	myosin alkali light chain 1, fast skeletal muscle, form 1	301	1e-81
			AAA59854.1	myosin light chain	301	1e-81
			CAB42846.1	myosin light chain-1	300	3e-81
			NP_524146.1	fast skeletal myosin alkali light chain 1 isoform 3f; A1 catalytic; A2 catalytic	272	4e-73
			P06741	MLE3_HUMAN Myosin light chain 3, skeletal muscle isoform (A2 catalytic)(Alkali) (MLC3F)	272	4e-73
			MOHUA2	myosin alkali light chain 1, fast skeletal muscle, form 2	272	4e-73
			CAA29020.1	MLC-3 (AA 1 - 150)	272	4e-73
			AA59885.1	myosin light chain	272	4e-73
			AAH05318.1	AAH05318 Unknown (protein for MGC:12401)	272	4e-73
			1607304A	myosin alkali L 3F	272	4e-73
			1405342A	ventricular myosin L1	239	5e-63
			2001201A	myosin:SUBUNIT=light chain:ISOTYPE=V/5B	238	9e-63
			CAA30292.1	ventricular myosin light chain 1 (AA 1 - 195)	238	9e-63
			NP_000249.1	myosin light chain 3	238	9e-63

			P08590	MLEV_HUMAN Myosin light chain 1, slow-twitch muscle Biventricular isoform (MLC1SB) (Alkali)	238	9e-63
			MOHUV	myosin alkali light chain 3, ventricular and slow skeletal muscle	238	9e-63
			AAA5985.1	myosin light chain	238	9e-63
			AAA59851.1	MLC-1V/Sb isoform	238	9e-63
			AAH09790.1	AAH09790 myosin, light polypeptide 3, alkali, ventricular, skeletal, slow	238	9e-63
			1607304B	myosin alkali L1Sb	238	9e-63
			AAF91089.1	AF174483_1 cardiac myosin light chain-1	238	9e-63
			NP_002486.1	myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch muscle A isoform	234	1e-61
			P14649	MLEV_HUMAN Myosin light chain 1, slow-twitch muscle A isoform (MLC1sa) (Alkali)	234	1e-61
			MOHUSA	myosin alkali light chain, slow skeletal muscle	234	1e-61
			CAA34457.1	myosin alkali light chain (AA 1-208)	234	1e-61
			AAA36320.1	myosin light chain 1 slow	234	1e-61
			AAH12425.1	AAH12425 Similar to myosin, light polypeptide 1, alkali, skeletal, fast	234	1e-61
			AAH14400.1	AAH14400 Similar to myosin, light polypeptide 1, alkali, skeletal, fast	234	1e-61
			NP_002487.1	atrial/embryonic alkali myosin light chain; myosin, atrial/fetal muscle, light chain	234	2e-61
			P12829	MLEF_HUMAN Myosin light chain 1, embryonic muscle/atrial isoform (PRO1957)	234	2e-61
			MOHU4E	myosin alkali light chain 4, embryonic and atrial	234	2e-61
			CAA32137.1	myosin alkali light chain (AA 1-197)	234	2e-61
			AAA36319.1	embryonic myosin alkali light chain (MLC1)	234	2e-61
			AAA59858.1	embryonic/atrial myosin light chain (MLC-1-emb/A isoform)	234	2e-61
			CAA41655.1	myosin alkaline light chain	234	2e-61
			AAF1098.1	AF16721_76 PRO1957	234	2e-61
			AAH30228.1	myosin, light polypeptide 4, alkali, atrial, embryonic	234	2e-61

NM_009477						uridine phosphorylase		473 e-133
NP_033503.1	Mm.4610	F:(H-D) +2.63	NP_003355.1	Q16831		UDP_HUMAN Uridine phosphorylase (UDRPase)		473 e-133
				JC4343		uridine phosphorylase (EC 2.4.2.3)		473 e-133
				CAA62369.1		uridine phosphorylase		473 e-133
				AAH01405.1		AAH01405 uridine phosphorylase		473 e-133
				AAH07348.1		AAH07348 uridine phosphorylase		473 e-133
				NP_775491.1		liver-specific uridine phosphorylase		371 e-102
				AAD12227.1		similar to uridine phosphorylase; similar to Q16831 (PID:g2494059)		371 e-102
				AAH33529.1		Similar to uridine phosphorylase		371 e-102
				AAH47030.1		Similar to uridine phosphorylase		263 4e-70
NM_009318		F:(H-D)	NP_003181.3			tapasin isoform 1 precursor; TAP-binding protein; TAP-associated protein		548 e-156
NP_033344.1	Mm.14097	+2.59	CAB09991.1			cICF0811.3.1 (TAP-binding protein (tapasin), isoform 1)		548 e-156
			BAA28757.1			Tapasin*02		548 e-156
			O15533			TPSN_HUMAN Tapasin precursor (TPSN) (TPN) (TAP-binding protein) (TAP-associated protein) (NGS-17)		548 e-156
			AAC20076.1			tapasin		548 e-156
			AAB82949.1			tapasin		548 e-156
			CAA73909.1			TAP-associated protein, TAP-A		548 e-155
			NP_757346.1			tapasin isoform 3 precursor; TAP-binding protein; TAP-associated		534 e-151
			CAC88185.1			cICF0811.3.3 (TAP-binding protein (tapasin), isoform 3)		534 e-151
			AAC33061.1			AF314222_1 tapasin		533 e-151
			NP_757345.1			tapasin isoform 2 precursor; TAP-binding protein; TAP-associated protein		353 4e-97
			CAC88184.1			cICF0811.3.2 (TAP-binding protein (tapasin), isoform 2)		353 4e-97
			AAD32924.2			AF067286_1 tapasins		352 5e-97

				BAA28759.1	Tapasin*02	226	7e-59
				BAA28758.1	Tapasin*01	225	1e-58
NM_026853				NP_543148.1	ankyrin repeat and SOCS box-containing protein 11; ankyrin repeat domain-containing SOCS box protein ASB11	481	e-136
	Mm.33225	F:(C-HI)+3.77		QBWXH4	Ankyrin repeat and SOCS box containing protein 11 (ASB-11)	481	e-136
				AAL60519.1	ankyrin repeat domain-containing SOCS box protein ASB11	481	e-136
				NP_543150.1	ankyrin repeat and SOCS box-containing protein 5; SOCS box protein ASB-5	303	3e-82
				QBWWX0	Ankyrin repeat and SOCS box containing protein 5 (ASB-5)	303	3e-82
				AAL18248.1	SOCS box protein ASB-5	303	3e-82
				BAC04791.1	unnamed protein product	303	3e-82
				BAC05382.1	unnamed protein product	303	3e-82
				AAH13172.1	Similar to DKFZP564L0862 protein	276	6e-74
				NP_076992.1	ankyrin repeat and SOCS box-containing 9	230	3e-60
				BAA91302.1	unnamed protein product	230	3e-60
				T12477	hypothetical protein DKFZb564L0862.1	228	1e-59
				CAB45708.1	hypothetical protein	228	1e-59
				AAH01244.1	Unknown (protein for MGC:4954)	212	8e-55
				NP_078977.2	ankyrin repeat and SOCS box-containing protein 13; ankyrin repeat domain-containing SOCS box protein Asb-13	197	3e-50
				QBWXK3	Ankyrin repeat and SOCS box containing protein 13 (ASB-13)	197	3e-50
				AAL57350.1	ankyrin repeat domain-containing SOCS box protein Asb-13	196	4e-50
		F:(C-HI)+3.26					
AB035725		F:(C-D)+2.96					
BAA88342.1	Mm.27972			AAD38198.1	AF155588_1 NSAP1 protein	852	0
				NP_006363.3	NS1-associated protein 1	852	0
				AAC12926.1	Gry-rbp	852	0
				AAK59703.1	hnRNP Q3	852	0

			AAK59705.1	hnRNP Q1		852	0
			AAH32643.1	Similar to NS1-associated protein 1		763	0
			AAK59704.1	hnRNP Q2		761	0
			NP_005817.1	heterogeneous nuclear ribonucleoprotein R		722	0
			O43390	ROR_HUMAN Heterogeneous nuclear ribonucleoprotein R (hnRNP R)		722	0
			T02673	heterogeneous nuclear ribonucleoprotein R		722	0
			AAK39540.1	heterogeneous nuclear ribonucleoprotein R		722	0
			AAH01449.1	heterogeneous nuclear ribonucleoprotein R		717	0
			XP_001541.2	heterogeneous nuclear ribonucleoprotein R		606	e-173
			AAH40844.1	Similar to apobec-1 complementation factor		530	e-151
			AAH21973.1	RNA-binding protein		338	3e-92
AK007264		F:(C-HI)					
BAB24924.1	Mm.200370	+3.24	NP_775491.1	liver-specific uridine phosphorylase		447	e-125
			AAD12227.1	similar to uridine phosphorylase; similar to Q16831 (PID:g2494059)		447	e-125
			AAH33529.1	Similar to uridine phosphorylase		447	e-125
			NP_003355.1	uridine phosphorylase		316	2e-86
			Q16831	UDP_HUMAN Uridine phosphorylase (UDRPase)		316	2e-86
			JC4343	uridine phosphorylase (EC 2.4.2.3)		316	2e-86
			CAA62369.1	uridine phosphorylase		316	2e-86
			AAH01405.1	AAH01405 uridine phosphorylase		316	2e-86
			AAH07348.1	AAH07348 uridine phosphorylase		316	2e-86
			AAH47030.1	Similar to uridine phosphorylase		205	6e-53
AK010640							
BAC25310.1	Mm.5875	F:(C-HI)					
		+3.21	NP_002764.1	prolactin preprolactin; protease, serine, 8		357	3e-98
			Q16651	PSS9_HUMAN Prostatein precursor		357	3e-98
			A57014	prostatein (EC 3.4.21.-) precursor		357	3e-98
			AAH41759.1	prostatein		357	3e-98

				AA119071.1	prolactin	357	3e-98
				AAH01462.1	protease, serine, 8 (prolactin)	357	3e-98
				2208326A	prolactin	357	3e-98
				NP_114154.1	marapsin; channel-activating protease 2	166	5e-56
				Q9BQR3	MPN_HUMAN Marapsin precursor	166	5e-56
				CAC35467.1	marapsin	166	5e-56
				BAB85497.1	serine protease 27	166	5e-56
				AAK38168.1	pancreatin	166	5e-56
				NP_071402.1	protease, serine, 22; brain-specific serine protease 4; protease, serine S1 family member 22; tyrosine epsilon	147	2e-51
				Q9GZV4	BSS4_HUMAN Brain-specific serine protease 4 precursor (BSSP-4) (SP001LA)	147	2e-51
				AAK35070.1	AF321182_1 serine protease PRSS22	147	2e-51
				BAB20263.1	brain-specific serine protease-4	147	2e-51
				AAH09726.1	protease, serine, 22	147	2e-51
				AAK33671.1	SP001LA	147	2e-51
					hexosaminidase A preproprotein; beta-N-acetylhexosaminidase; N-acetyl-beta-glucosaminidase	922	0
NM_010421				NP_000511.1	HEXA_HUMAN Beta-hexosaminidase alpha chain precursor (N-acetyl-beta-glucosaminidase) (Beta-N-acetylhexosaminidase) (Hexosaminidase A)	922	0
				P06865	beta-N-acetylhexosaminidase (EC 3.2.1.52) alpha chain precursor	922	0
				A0HUBA	beta-hexosaminidase alpha chain	922	0
				AAK00965.1	beta-hexosaminidase alpha chain	922	0
				AAD13932.1	1680052_1 lysosomal enzyme beta-N-acetylhexosaminidase A	922	0
				AAH18927.1	hexosaminidase A (alpha polypeptide)	922	0
				AAA51827.1	N-acetyl-alpha-glucosaminidase prepro-polypeptide	890	0
				AAH01138.1	Similar to hexosaminidase A (alpha polypeptide)	764	0
				AAA51828.1	N-acetyl-beta-glucosaminidase prepro-polypeptide	602	e-172

				AAA68620.1	beta-hexosaminidase beta-subunit	602	e-172
				NP_000512.1	hexosaminidase B preproprotein; N-acetyl-beta-glucosaminidase	602	e-172
					HEXB_HUMAN Beta-hexosaminidase beta chain precursor (N-acetyl-beta-glucosaminidase) (Beta-N-acetylhexosaminidase) (Hexosaminidase B)		
				P07686		602	e-172
				A31250	beta-N-acetylhexosaminidase (EC 3.2.1.52) beta chain precursor	602	e-172
				AAA62645.1	beta-hexosaminidase beta-subunit	602	e-172
				AAH17378.1	hexosaminidase B (beta polypeptide)	602	e-172
				AAM46114.1	AF378118_1 cervical cancer proto-oncogene 7	602	e-172
AK008434							
NP_666245.1	Mm.21218	F:(C-HI) +3.08		GPP34-related protein		406	e-113
				CAC13125.1	GPP34-related protein	406	e-113
				AAH13870.1	GPP34-related protein	406	e-113
				BAA91750.1	unnamed protein product	335	6e-92
					golgi phosphoprotein 3; golgi protein; golgi peripheral membrane protein 1, 34 kDa; golgi-associated protein; coat-protein	310	2e-84
				NP_071413.1		310	2e-84
				CAC13124.1	Golgi protein	310	2e-84
				AAH12123.1	golgi phosphoprotein 3	310	2e-84
				AAH33725.1	golgi phosphoprotein 3 (coat-protein)	310	2e-84
				BAC11438.1	unnamed protein product	310	2e-84
				T42877	hypothetical protein DKFZp434P1217.1	269	7e-72
				CAB61398.1	hypothetical protein	269	7e-72
				NP_036599.1	SNARE associated protein snapin	230	3e-60
				AAD11417.1	snapi	230	3e-60
				BAB14927.1	unnamed protein product	230	3e-60
				AAH00761.1	SNARE associated protein snapin	230	3e-60
				AAH04494.1	SNARE associated protein snapin	230	3e-60
NM_011429							
NP_598615.1	Mm.28793	F:(C-HI) +3.07				230	3e-60

NM_011710		F:(C-H)		SVW_HUMAN_Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TRPRS) (IFP53) (nWRS)	860	0
NP_035840.1	Mm.38433	+2.94	P23381	tryptophan-tRNA ligase (EC 6.1.1.2) [similarity]	860	0
			A41706	471 aa polypeptide (gamma2)	860	0
			CAA42545.1	transfer RNA-Trip synthetase	860	0
			AAA67324.1	Unknown (protein for MGC:15973)	860	0
			AAH17489.1	unnamed protein product	860	0
			CAD62335.1	IFP53	868	0
			CAA44450.1	tryptophanyl-tRNA synthetase; interferon-induced protein 53	854	0
			NP_004175.1	transfer RNA-Trip synthetase	854	0
			AA61298.1	tryptophanyl-tRNA synthetase 1	554	e-157
			CAB94199.1	tryptophanyl-tRNA synthetase	226	6e-59
			CAB94198.1	MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)	336	4e-92
NM_008578		F:(C-H)		MEFB_HUMAN_MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2)	336	4e-92
NP_032604.1	Mm.844	+2.85	NP_005910.1	serum response factor-related protein 2	336	4e-92
			Q02080	serum response factor-related protein	336	4e-92
			A39481	myocyte-specific enhancer factor 2 (XMEF2)	336	4e-92
			CAA44978.1	XMEF2	336	4e-92
			CAA46515.1	serum response factor-related protein F2	336	4e-92
			AA86982.1		336	4e-92
			1804266C		336	4e-92
NM_013771		F:(C-H)		YMB1-like 1 isoform 3; ATP-dependent metalloprotease FtsH1 homolog	1341	0
NP_038799.1	Mm.23355	+2.75	NP_053078.1	ATP-dependent metalloprotease YMB1L	1341	0
			CAB51858.1	YMB1-like 1 (S. cerevisiae)	1341	0
			AAH24032.1	YMB1-like 1 (S. cerevisiae)	1341	0
			AAE23507.1	YMB1-like 1 isoform 1; ATP-dependent metalloprotease FtsH1 homolog	1286	0

				AAK57555.1	AF151782_1 ATP-dependent metalloprotease FtsH1 homolog	1285	0
				NP_647474.1	YME1-like 1 isoform 2; ATP-dependent metalloprotease FtsH1 homolog	1224	0
				AAH07795.1	AAH07795 Similar to YME1-like 1 (S. cerevisiae)	1224	0
				AAD20962.1	FtsH homolog	992	0
				CAB99462.1	putative ATPases	991	0
				CAC19650.1	ba145B8.2 (YME1 (S. cerevisiae)-like 1)	842	0
				AAH24282.1	Similar to AFG3 ATPase family gene 3-like 2 (yeast)	354	4e-97
				NP_006787.1	AFG3 ATPase family gene 3-like 2; AFG3 (ATPase family gene 3, yeast)-like 2; ATPase family gene 3-like 2; ATPase family gene 3, yeast	352	1e-96
				Q9Y4W6	AF32_HUMAN AFG3-like protein 2 (Paraplegin-like protein)	352	1e-96
				CAB48398.1	paraplegin-like protein	352	1e-96
				NP_003110.1	paraplegin	312	2e-84
				CAA76314.1	paraplegin	312	2e-84
				Q9UHI5	LAT2_HUMAN Large neutral amino acids transporter small subunit 2 (L-type amino acid transporter 2) (hLAT2)	880	0
NM_016972			F:(C-HI)	AAF20381.1	AF171669_1 glycoprotein-associated amino acid transporter LAT2	880	0
NP_058698.1	Mm_27830			BAB21519.1	L-type amino acid transporter 2	880	0
				NP_036376.1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	875	0
				CAB40137.1	SLC7A8 protein	875	0
				AAF05895.1	F135828_1 L amino acid transporter-2; LAT-2	659	0
				CAB2816.1	unnamed protein product	640	0
				NP_062823.1	solute carrier family 7, member 10; asc-type amino acid transporter 1	619	e-177
				Q9NS82	AAA1_HUMAN Asc-type amino acid transporter 1 (Asc-1)	619	e-177
				BAB03213.1	asc-type amino acid transporter 1	619	e-177

		AAK93960.1	AF340165_1 amino acid transporter	619 e-177
		CAC81900.1	ASC1 protein	619 e-177
		AAH35627.1	similar to solute carrier family 7	619 e-177
		AAF05897.1	AF135830_1 L amino acid transporter-2; LAT-2	546 e-155
		AAC61479.1	amino acid transporter E16	480 e-129
			solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 5; Membrane protein E16; Solute carrier family 7, member 5; 4F2 light chain	
		NP_003477.2		458 e-128
			LAT1_HUMAN Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 light chain) (4F2LC) (CD98 light chain) (Integral membrane protein E16) (hLAT1)	458 e-128
		Q01650		458 e-128
		JG0165	LAT1 protein	458 e-128
		BAA33851.1	CD98 light chain	458 e-128
		AAD20464.1	L-type amino acid transporter subunit	458 e-128
		BAA84648.1	L-type amino acid transporter 1	458 e-128
		AAH42600.1	Similar to solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 5	458 e-128
		BAF70708.1	sodium-independent neutral amino acid transporter LAT1	457 e-128
		AAH39692.1	Similar to solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 5	457 e-128
			lactate dehydrogenase B	648
NM_008492	F:(C-H)	NP_002291.1	LDHB_HUMAN L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H)	0
NP_032518.1	Mm.9745	P07195		0
		DEHULH	L-lactate dehydrogenase (EC 1.1.1.27) chain H	848

		CAA68701.1	lactate dehydrogenase B (AA 1 - 334)	648	0
		CAA32033.1	lactate dehydrogenase B	648	0
		AAH02362.1	AAH02362 lactate dehydrogenase B	648	0
		AAH15122.1	AAH15122 lactate dehydrogenase B	648	0
		110Z	A Chain A, Human Heart L-Lactate Dehydrogenase H Chain, Ternary Complex With NADH And Oxamate	646	0
		110Z	B Chain B, Human Heart L-Lactate Dehydrogenase H Chain, Ternary Complex With NADH And Oxamate	646	0
		NP_005557.1	lactate dehydrogenase A ^{1,45}	519	e-147
		P00338	LDHA_HUMAN L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M)	519	e-147
		DEHULM	L-lactate dehydrogenase (EC 1.1.1.27) chain M	519	e-147
		CAA26088.1	lactate dehydrogenase-A	519	e-147
		CAA26879.1	lactate dehydrogenase-A	519	e-147
		1110	A Chain A, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary Complex With NADH And Oxamate	517	e-146
		1110	B Chain B, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary Complex With NADH And Oxamate	517	e-146
		1110	C Chain C, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary Complex With NADH And Oxamate	517	e-146
		1110	D Chain D, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary Complex With NADH And Oxamate	517	e-146
		1110	E Chain E, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary Complex With NADH And Oxamate	517	e-146
		1110	F Chain F, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary Complex With NADH And Oxamate	517	e-146

				III10	G Chain G, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary Complex With Nadh And Oxamate	517	e-148
				III10	H Chain H, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary Complex With Nadh And Oxamate	517	e-146
				AAA59507.1	lactate dehydrogenase (E.C. 1.1.1.27)	476	e-134
				NP_002292.1	lactate dehydrogenase C	476	e-134
				NP_059144.1	lactate dehydrogenase C	476	e-134
				AAA21348.1	lactate dehydrogenase-C	476	e-134
				AAH19249.1	AAH19249 lactate dehydrogenase C	476	e-134
				P07864	LDHC HUMAN L-lactate dehydrogenase C chain (LDH-C) (LDH testis subunit) (LDH-X)	476	e-134
				DEHULC	L-lactate dehydrogenase (EC 1.1.1.27) chain X	476	e-134
				NP_149972.1	lactate dehydrogenase A -like	460	e-129
				Q9BYZ2	LDHL_HUMAN L-lactate dehydrogenase A-like	480	e-129
				AAG49399.1	lactate dehydrogenase A	460	e-129
				BAB71710.1	unnamed protein product	459	e-129
				AAH22034.1	AAH22034 lactate dehydrogenase A -like	459	e-129
				AAA59508.1	lactate dehydrogenase-C	410	e-114
				F(C-HI) +2.71	kallikrein 6 preproprotein; protease M; protease, serine, 9; neurosin; zyme	366	e-101
NM_011177 NP_035307.1	Mm.3944			NP_002765.1	KLK6_HUMAN Kallikrein 6 precursor (Protease M) (Neurosin) (Zyme) (SP59)	366	e-101
				Q92876	protease M	366	e-101
				AAB07113.1	neurosin	366	e-101
				BAA11306.1		366	e-101

				serine protease	366	e-101
				AF149289_1 kallikrein-like serine protease; zyme; protease M; neurosin	366	e-101
				AF243527_1 protease M	366	e-101
				AAH15525 kallikrein 6 (neurosin, zyme)	366	e-101
				A Chain A, Human Prokallikrein 6 (Hk6) PROZYME PROTEASE M	347	1e-95
				Proneurosin	346	4e-95
				A Chain A, Human Kallikrein 6 (Hk6) Active Form With Benzamidase Inhibitor	346	4e-95
				A Chain A, Human Kallikrein 6 (Hk6) Active Form With Benzamidase Inhibitor At 1.56 A Resolution	346	4e-95
				kallikrein 8 isoform 1 preproprotein; protease, serine, 19; neurosin; ovasin; tumor-associated differentially expressed gene 14	241	2e-63
				NP_009127.1		
				KLK8_HUMAN Neuropilin precursor (NP) (Kallikrein 8) (Ovasin) (Serine protease TADG-14) (Tumor-associated differentially expressed gene-14 protein)	241	2e-63
				O60259	241	2e-63
				BAA28673.1	241	2e-63
				neuropilin	241	2e-63
				AF095742_1 serine protease ovasin	241	2e-63
				serine protease ovasin	241	2e-63
				AAD29574.1	241	2e-63
				serine protease ovasin	241	2e-63
				BAA82665.1	241	2e-63
				neuropilin type	241	2e-63
				AAD56050.1	241	2e-63
				AF053982_1 serine protease TADG14	241	2e-63
				AAC33361.1	241	2e-63
				AF243527_9 neuropilin	241	2e-63
				Unknown (protein for MGC:50513)	240	3e-63
				kallikrein 8 isoform 2; protease, serine, 19; neurosin; ovasin; tumor-associated differentially expressed gene 14	238	8e-63
				NP_653088.1	238	8e-63
				BAA82666.1	238	8e-63
				neuropilin type2	238	8e-63
				NP_071329.1	238	1e-62
				kallikrein 14 preproprotein; kallikrein-like protein 6		

			Q9P0G3	KLKB_HUMAN Kallikrein 14 precursor (Kallikrein-like protein 6) (KLK-L6)	238	1e-62
			AAD50773.2	AF161221_1 kallikrein-like protein 6	238	1e-62
			AAG23260.1	AC011473_7 Homo sapiens kallikrein-like protein 6	238	1e-62
			AAK48523.1	AF283669_1 kallikrein 14	238	1e-62
			AAK48524.1	AF283670_1 kallikrein 14	238	1e-62
			AAG33354.1	AF243527_2 ACO protease	228	1e-59
			NP_059979.2	kallikrein 15 isoform 4 preproprotein; ACO protease; prostinog kallikrein-like serine protease	227	3e-59
			Q9H2R5	KLKF_HUMAN Kallikrein 15 precursor (ACO protease)	227	3e-59
			AAG09469.1	AF242195_1 KLK15	227	3e-59
			AAK62813.1	AF303046_1 prostinogen	226	6e-59
NM_010123 NP_034253.1	Mm.2238	F:(C-H) +2.69	NP_003741.1	eukaryotic translation initiation factor 3, subunit 10 (theta, 50/170kDa; eukaryotic translation initiation factor 3, subunit 10 (theta, 170kD); Eukaryotic translation initiation factor 3, subunit 10, 170kD; eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD)	474	e-162
			Q14152	IF3A_HUMAN Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (eIF3 p167) (eIF3 p180) (eIF3 p185) (eIF3a)	474	e-162
			BAA09488.1	The KIAA0139 gene product is related to mouse centrosomin B.	474	e-162
			AAB41584.1	p167	474	e-162
			AAB80695.1	translation initiation factor 3 large subunit	474	e-162
NM_010068 NP_034198.1	Mm.89772	F:(C-H) +2.67	NP_787045.1	DNA cytosine-5 methyltransferase 3 beta isoform 3; DNA methyltransferase HsaIIIB; DNA MTase HsaIIIB	1201	0
			CAB53069.1	dJ1085F17.1.3 (DNA Cytosine-5 Methyltransferase 3 beta, isoform 3)	1201	0
			AAD53062.1	AF156487_1 DNA cytosine-5 methyltransferase 3 beta 3	1201	0

			NP_787046.1	DNA cytosine-5 methyltransferase 3 beta isoform 6; DNA methyltransferase HsallIB; DNA MTase HsallIB	1108	0
			AAF04015.1	AF176228_1 DNA cytosine-5 methyltransferase 3B	1108	0
			NP_787044.1	DNA cytosine-5 methyltransferase 3 beta isoform 2; DNA methyltransferase HsallIB; DNA MTase HsallIB	1105	0
			ICAB53071.1	dJ1085F17.1.2 (DNA Cytosine-5 Methyltransferase 3 beta, isoform 2)	1105	0
			NP_008823.1	DNA cytosine-5 methyltransferase 3 beta isoform 1; DNA methyltransferase HsallIB; DNA MTase HsallIB	1093	0
			Q9UBC3	DM3B_HUMAN DNA (cytosine-5)-methyltransferase 3B (Dnmt3b) (DNA methyltransferase HsallIB) (DNA MTase HsallIB) (M.HsallIB)	1093	0
			CAB53070.1	dJ1085F17.1.1 (DNA Cytosine-5 methyltransferase 3 beta, isoform 1)	1093	0
			AAD53063.1	AF156488_1 DNA cytosine-5 methyltransferase 3 beta 1	1093	0
			AAL57040.1	AF331857_1 DNA cytosine methyltransferase 3 beta	1093	0
			Q9Y6K1	DM3A_HUMAN DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase HsallIA) (DNA MTase HsallIA) (M.HsallIA)	662	0
			AAL57039.1	AF331856_1 DNA cytosine methyltransferase 3 alpha	662	0
			NP_072046.2	DNA cytosine methyltransferase 3 alpha isoform a; DNA methyltransferase HsallIA; DNA MTase HsallIA; DNA cytosine methyltransferase 3A2	662	0
			NP_783328.1	DNA cytosine methyltransferase 3 alpha isoform a; DNA methyltransferase HsallIA; DNA MTase HsallIA; DNA cytosine methyltransferase 3A2	662	0
			AAD33084.2	AF067972_1 DNA cytosine methyltransferase 3 alpha	662	0
			AAH43617.1	DNA (cytosine-5)-methyltransferase 3 alpha	662	0
			NP_715640.1	DNA cytosine methyltransferase 3 alpha isoform b; DNA methyltransferase HsallIA; DNA MTase HsallIA; DNA cytosine methyltransferase 3A2	662	0
			AAH40037.1	AF480163_1 DNA cytosine methyltransferase 3A2	662	0
			AAH18214.1	AAH18214 Unknown (protein for IMAGE3862699)	297	9e-80

					NP_787063.1	tyrosine-5-methyltransferase 3-like protein isoform 2; cytosine-5-methyltransferase 3-like protein; human cytosine-5-methyltransferase 3-like protein	268	6e-71
					AAD31434.1	DNA methyltransferase 3 beta 5	227	2e-70
NM_013506					AAH13708.1	AAH13708 Unknown (protein for MGC:21863)	759	0
NP_038534.1	Mm.16323	F:(C-H) +2.65			AAH15842.1	AAH15842 Unknown (protein for MGC:27241)	757	0
					NP_001958.1	eukaryotic translation initiation factor 4A, isoform 2	755	0
					Q1424	IF42_HUMAN Eukaryotic Initiation factor 4A-II	755	0
					BAA06336.1	eukaryotic initiation factor 4AII	755	0
					AAH12547.1	AAH12547 Similar to eukaryotic translation initiation factor 4A2	754	0
					NP_001407.1	eukaryotic translation initiation factor 4A, isoform 1	686	0
					P04765	IF41_HUMAN Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I)	686	0
					S33681	translation initiation factor eIF-4A.I	686	0
					BAA02897.1	eukaryotic initiation factor 4AI	686	0
					AAH09585.1	AAH09585 eukaryotic translation initiation factor 4A, isoform 1	686	0
					AAH06210.1	AAH06210 Similar to eukaryotic translation initiation factor 4A, isoform 1	583 e-166	
					AAH06380.1	AAH06380 Unknown (protein for IMAGE:4099982)	578 e-164	
					AAF64266.1	AF208852_1 BM-010	529 e-150	
					S45142	translation initiation factor eIF-4A2 homolog	510 e-144	
					CAA56074.1	translation initiation factor	510 e-144	
					NP_055555.1	KIAA0111 gene product	509 e-144	
					P38919	IP4N_HUMAN Eukaryotic initiation factor 4A-like NUK-34	509 e-144	
					BAA04879.1	KIAA0111	509 e-144	
					AAH03662.1	AAH03662 KIAA0111 gene product	509 e-144	
					AAH04386.1	AAH04386 KIAA0111 gene product	509 e-144	

			AAH11151.1	AAH11151.1 Similar to KIAA0111 gene product	509 e-144	
NM_008218		F:(C-HI) +2.64				
NP_032244.1	Mm.198110	F:(HLD) +2.99	AAK37554.1	AF349571.1 hemoglobin alpha-1 globin chain	255	3e-68
			NP_000508.1	alpha 2 globin	254	7e-68
			NP_000549.1	alpha 1 globin	254	7e-68
			P01922	HBA HUMAN Hemoglobin alpha chain	254	7e-68
			HAHU	hemoglobin alpha chain [validated]	254	7e-68
			1BZ1	A Chain A, Hemoglobin (Alpha + Met) Variant	254	7e-68
			1BZ1	C Chain C, Hemoglobin (Alpha + Met) Variant	254	7e-68
			CAA23748.1	alpha globin	254	7e-68
			CAA23752.1	reading frame alpha-globin	254	7e-68
			AAB59407.1	hba2 alpha globin	254	7e-68
			AAB59408.1	hba1 alpha globin	254	7e-68
			CAB06354.1	alpha-globin 1	254	7e-68
			CAB06355.1	alpha-globin 2	254	7e-68
			AAC72839.1	alpha-2 globin	254	7e-68
			AAC97373.1	alpha one globin	254	7e-68
			AAH05931.1	AAH05931 hemoglobin, alpha 2	254	7e-68
			AAH08572.1	AAH08572 hemoglobin, alpha 2	254	7e-68
			AAK61215.1	AE006462.7 HBA2	254	7e-68
			AAK61216.1	AE006462.8 HBA1	254	7e-68
			AAH32122.1	hemoglobin, alpha 2	254	7e-68

				AA083102.1	AF525460_1 alpha-1-globin		254	7e-88
				AA072612.1	AF230076_1 alpha-2-globin		253	1e-67
				AA004486.1	hemoglobin alpha2		253	1e-67
				IC7D	A Chain A, Deoxy Rbb1.2 (Recombinant Hemoglobin)		252	2e-67
				IC7C	A Chain A, Deoxy Rbb1.1		252	2e-67
				IOIP	A Chain A, Deoxy Hemoglobin		252	2e-67
					A Chain A, Hemoglobin Thionville Alpha Chain Mutant With Val 1 Replaced By Glu And An Acetylated Met Bound To The Amino Terminus		251	3e-67
				IBAB	C Chain C, Hemoglobin Thionville Alpha Chain Mutant With Val 1 Replaced By Glu And An Acetylated Met Bound To The Amino Terminus		251	3e-67
					homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1; MMS-inducible gene		592	e-169
				NP_055500.1	HERP_HUMAN Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein (Methyl methanesulphonate (MMF)-inducible fragment protein 1)		592	e-169
				Q15011			592	e-169
				BA003521.1	unknown		592	e-169
				AAC09355.1	stress protein Herp		592	e-169
				BAB07891.1	stress protein Herp		592	e-169
				BAB19010.1	stress protein Herp		592	e-169
				AAH00086.1	AAH00086 homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1		592	e-169
				AAH08320.1	AAH08320 homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1		592	e-169

NM_022331
NP_071728.1 Mm.29151
F:(C-H)
+2.58

				AAH29673.1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	592 e-189
				AAC09387.1	unknown	525 e-148
				AAG17233.1	AF217890_1 unknown	295 2e-79
				AAH09739.1	AAH09739 Similar to homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	218 2e-56
NM_023719					VDUP1	761 0
NP_076208.1	Mm.77432	F:(C-HI) +2.57		BAB18859.1	2019235A	761 0
				NP_006463.2	thioredoxin interacting protein; upregulated by 1,25-dihydroxyvitamin D-3	760 0
				AAH31977.2	brain-expressed HHCPA78 homolog VDUP1	760 0
				AAH28704.1	Unknown (protein for IMAGE:4838787)	326 9e-88
				XP_041721.2	similar to RIKEN cDNA 2410003C09 [Mus musculus]	328 9e-88
				BA02614.1	KIAA1378 protein	306 7e-83
				XP_033042.2	similar to hypothetical protein CLONE24945	304 5e-82
				AAH15928.1	AAH15928 Unknown (protein for MGC:8773)	304 5e-82
				NP_056498.1	hypothetical protein CLONE24945	256 2e-67
				AAG32479.1	AF193051_1 unknown	256 2e-67
				AAH22516.1	Unknown (protein for MGC:26574)	254 4e-67
				AAD20053.1	Unknown	214 7e-55
NM_016741					membrane glycoprotein CLA-1 protein long form precursor	816 0
NP_058021.1	Mm.4603	F:(C-HI) +2.57		A48528	CLA-1	816 0
				CA080277.1	scavenger receptor class B, member 1; CD36 antigen-like 1; scavenger receptor class B type 1; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1	749 0
				NP_005496.2	AAH22087 Similar to CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1	749 0
				AAH22087.1		749 0

				A66525	lysosomal integral membrane protein II	277	4e-74
					scavenger receptor class B, member 2; CD36 antigen (collagen type I receptor, thrombospondin receptor) -; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)	277	6e-74
				NP_005497.1		277	6e-74
				Q14108	LY71 HUMAN Lysosome membrane protein II (LIMP II) (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2)	277	6e-74
				BAA02177.1	85kDa lysosomal sialoglycoprotein	277	6e-74
				AAH21892.1	AAH21892 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)	277	6e-74
				P16671	CD36 HUMAN Platelet glycoprotein IV (GPIV) (GPIIb) (CD36 antigen) (PAS IV) (PAS-4 protein)	244	3e-64
				A54870	cell adhesion receptor CD36	244	3e-64
				AAA35534.1	CD36 antigen	244	3e-64
				AAA58412.1	antigen CD36	244	3e-64
				AAA58413.1	antigen CD36	244	3e-64
				CAA83662.1	CD36	244	3e-64
				AAH08406.1	AAH08406 CD36 antigen (collagen type I receptor, thrombospondin receptor)	244	3e-64
				2015709A	85kD protein	244	3e-64
					CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36 antigen (collagen type I); cluster determinant 36; fatty acid translocase; scavenger receptor class B, member 3	244	3e-64
				NP_000063.1	antigen CD36	244	3e-64
				AAA16068.1		244	3e-64
				AAD13993.1	S67532 I glycoprotein GPIIb/GPIV	239	1e-62

NM_007399				AAAM14636.1	CD36 antigen (collagen type I receptor, thrombospondin receptor)	230	8e-60
NP_031425.1	Mm.3911	F:(C-H) +2.55		NP_001101.1	a disintegrin and metalloprotease domain 10	1414	0
				AAC51766.1	ADAM10	1414	0
				CAA88463.1	disintegrin-metalloprotease MADM	1175	0
				S52920	disintegrin (EC 3.4.24.-)	923	0
				NP_003174.2	a disintegrin and metalloprotease domain 17 isoform 1 preproprotein;		
				NP_068604.1	TNF-alpha converting enzyme; snake venom-like protease	250	8e-66
				AAC39721.1	snake venom-like protease	250	8e-66
				NP_068604.1	a disintegrin and metalloprotease domain 17 isoform 2 preproprotein;		
				NP_068604.1	TNF-alpha converting enzyme; snake venom-like protease	248	2e-65
				AAB53014.1	TNF-alpha converting enzyme precursor	248	2e-65
				P78536	AD17_HUMAN ADAM 17 precursor (A disintegrin and metalloprotease domain 17) (TNF-alpha converting enzyme)		
				AAB51586.1	(TNF-alpha convertase) (Snake venom-like protease) (CD156b antigen)	248	2e-65
				AAB51514.1	TNF-alpha converting enzyme	248	2e-65
				AAB51514.1	TNF-alpha converting enzyme	248	2e-65
AK011472				AAH40436.1	Similar to splicing factor, arginine/serine-rich 11	296	3e-80
BAB27642.1	NULL	F:(C-H) +2.53		CAC04184.1	dJ677H15.2 (splicing factor, arginine/serine-rich 11)	296	3e-80
				NP_004759.1	splicing factor p54; arginine-rich 54 kDa nuclear protein	296	3e-80
				Q05519	SFRB_HUMAN Splicing factor arginine/serine-rich 11 (Arginine-rich 54 kDa nuclear protein) (p54)		
				A40988	54K arginine-rich nuclear protein	296	3e-80
				AAA35554.1	arginine-rich nuclear protein	296	3e-80

NM_008655					45B HUMAN Growth arrest and DNA-damage-inducible protein		
NP_032881.1	Mm.1360	F:(C-HI) +1.64	O75293	AAC34572.1	GADD45 beta Negative growth-regulatory protein MyD118 (Myeloid differentiation primary response protein MyD118)	288	1e-71
				AAC33328.1	MY18_HUMAN	288	1e-71
				AAG48366.1	growth arrest and DNA-damage-inducible protein GADD45beta	288	1e-71
				AAM97794.1	AF087853_1 growth arrest and DNA damage inducible protein beta	288	1e-71
				NP_056490.1	growth arrest and DNA-damage-inducible, beta	288	1e-71
				AAC36361.1	DKFZP566B133 protein; myeloid differentiation primary response; myeloid differentiation primary response gene	253	3e-67
AK003571				BAA74920.1	negative growth-regulatory protein MyD118	253	3e-67
XP_129443.2	Mm.40568	F:(C-HI) +1.62	XP_046751.3	KIAA0897 protein		483	e-136
				AAC28102.1	similar to liprin alpha 4 [Rattus norvegicus]	483	e-136
				AAC28100.1	liprin-alpha4	403	e-112
				AAC50172.1	liprin-alpha2	377	e-104
				NP_003617.1	LAR-interacting protein 1a	346	3e-95
				AAC50173.1	PTPRF interacting protein alpha 1 isoform b; LAR-interacting protein 1	348	3e-95
				AAH34046.1	LAR-interacting protein 1b	346	3e-95
				S55553	PPF1A1 protein	346	3e-95
				XP_027883.4	LAR-interacting protein LIP1b	346	3e-95
				BAA31629.2	similar to KIAA0654 protein	322	5e-88
AK013469				NP_699204.1	KIAA0654 protein	322	5e-88
BAC39584	Mm.177112	F:(C-HI) +1.53	NP_699204.1	AAH37567.1	hypothetical protein MGC45484	771	0
				AAH2526.1	Unknown (protein for MGC:45484)	771	0
					Similar to alanine-glyoxylate aminotransferase 2-like 1	593	e-169

				BAC03766.1	unnamed protein product	593 e-169
				NP_112569.1	alanine-glyoxylate aminotransferase 2-like 1	571 e-162
				CAC22283.1	alanine:glyoxylate aminotransferase 2 homolog 1, splice form 1	571 e-162
				NP_116310.1	hypothetical protein MGC15875	295 2e-79
				AAH08009.1	AAH08009 Unknown (protein for MGC:15875)	295 2e-79
				NP_114106.1	alanine-glyoxylate aminotransferase 2 precursor; beta-alanine-pyruvate aminotransferase; beta-ALAAAT II	258 2e-68
				Q8BYV1	AGT2_HUMAN Alanine-glyoxylate aminotransferase 2, mitochondrial precursor (AGT 2) (Beta-alanine-pyruvate aminotransferase) (Beta-ALAAAT II)	258 2e-68
				CAC24841.1	alanine-glyoxylate aminotransferase 2	258 2e-68
			F:(C-D)+ 8.51			
AK013950			F:(C-HI) +3.76	AAF36152.1	HSPC232	113 1e-52
NP_079929.1	Mm.38169					
NIM_009104			F:(C-D)+ 7.08	NP_001025.1	ribonucleotide reductase M2 polypeptide	694 0
NP_033130.1	Mm.99			P31350	Ribonucleoside-diphosphate reductase M2 chain (Ribonucleotide reductase small chain)	694 0
				S25854	ribonucleoside-diphosphate reductase (EC 1.17.4.1) small chain	694 0
				CAA42181.1	small subunit ribonucleotide reductase	694 0
				AAH01886.1	ribonucleotide reductase M2 polypeptide	694 0
				AAK51163.1	ribonucleotide reductase M2 subunit	694 0
				AAH30154.1	ribonucleotide reductase M2 polypeptide	694 0
				1706181A	ribonucleotide reductase	545 e-155
				XP_042096.1	similar to hypothetical protein DKFZp761E1312.1 - human (fragment)	534 e-151
				BAA92434.1	ribonucleotide reductase	534 e-151
				BAA92493.1	ribonucleotide reductase	534 e-151
				T46249	hypothetical protein DKFZp761E1312.1	534 e-151

				BAA92005.1	unnamed protein product	533 e-161
				AAH42948.1	Similar to ribonucleotide reductase M2 polypeptide	496 e-140
				AAH42488.1	Similar to ribonucleotide reductase M2 polypeptide	474 e-133
				AAH2932.1	Similar to ribonucleotide reductase protein 12 class I	309 8e-84
NM_010206					fibroblast growth factor receptor 1 isoform 1 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast protein; protein-tyrosine kinase; tyrosyl-protein kinase; hydroxyaryl-protein kinase	
NP_034336.1	Mm.3157	F:(C-D)+ 6.36		NP_000596.1	Basic fibroblast growth factor receptor 1 precursor (FGFR-1) (bFGF-R) (Fms-like tyrosine kinase-2) (c-fgr)	1562 0
				P11382	fibroblast growth factor receptor 1 precursor	1562 0
				TVHUG	fibroblast growth factor receptor 1 precursor	1562 0
				CAA37015.1	fibroblast growth factor receptor-FLG precursor	1562 0
				CAA40403.1	Fibroblast Growth Factor Receptor, 3-Ig Domain+2 AA Insert	1562 0
				CAA47375.1	fibroblast growth factor receptor	1562 0
				CAA38101.1	precursor polypeptide (AA-21 to 801)	1561 0
				AAA35958.1	heparin-binding growth factor receptor	1560 0
					fibroblast growth factor receptor 1 isoform 2 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosyl-protein kinase; hydroxyaryl-protein kinase	1555 0
				NP_056934.2	Fibroblast Growth Factor Receptor, 3 Ig-Domain Form	1555 0
				CAA40402.1	fibroblast growth factor receptor	1555 0
				AAA35840.1	Sec61 alpha form 1; sec61 homolog	931 0
NM_016806				NP_037468.1	S611_HUMAN Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1)	931 0
NP_058602.1	Mm.28375	F:(C-D)+ 5.39		P38378	sec61 homolog	931 0
				AAD39847.1	AF346602_1 Sec61 alpha form 1	931 0
				AAK29083.1		931 0

				Q9Y2R3	S612_HUMAN Protein transport protein Sec61 alpha subunit isoform 2 (Sec61 alpha-2)		909	0
				AAD21765.1	sec61 homolog; Sec61 alpha form 2		909	0
				NP_060614.2	sec61 homolog; Sec61 alpha form 2		891	0
				AAK29084.1	AF346603.1 Sec61 alpha form 2		891	0
				AAH02951.1	AAH02951 Similar to CG9539 gene product		828	0
				AAH26179.1	Similar to Sec61 alpha form 2		778	0
				BAB14148.1	unnamed protein product		775	0
				BAC11298.1	unnamed protein product		696	0
				BAA91692.1	unnamed protein product		432	e-121
				BAB13955.1	unnamed protein product		432	e-121
				CAD38592.1	hypothetical protein		425	e-119
				BAC11283.1	unnamed protein product		338	1e-92
				BAC11434.1	unnamed protein product		338	1e-92
NM_025673 NP_079949.1	Mm.22435	F:(C-D)+ 4.22 F:(C-H) +2.51		NP_071413.1	golgi phosphoprotein 3; golgi protein; golgi peripheral membrane protein 1, 34 kDa; golgi-associated protein; coat-protein		481	e-136
				CAC13124.1	Golgi protein		481	e-136
				AAH12123.1	golgi phosphoprotein 3		481	e-136
				AAH33725.1	golgi phosphoprotein 3 (coat-protein)		481	e-136
				BAC11438.1	unnamed protein product		481	e-136
				T42877	hypothetical protein DKFZp434P1217.1		416	e-116
				CAB61398.1	hypothetical protein		416	e-116
				NP_060648.2	GPP34-related protein		342	8e-94
				CAC13125.1	GPP34-related protein		342	8e-94
				AAH13870.1	GPP34-related protein		342	8e-94

				unnamed protein product	291	1e-78
NM_033037				cysteine dioxygenase	396	e-110
NP_149026.1	Mm.29996	F:(C-D)+ 3.88	BAA12872.1	cysteine dioxygenase, type I	395	e-110
			NP_001792.1	CYDX_HUMAN Cysteine dioxygenase type I (CDO) (CDO-I)	395	e-110
			S50192	cysteine dioxygenase (EC 1.13.11.20) type I	395	e-110
			CAA80552.1	cysteine dioxygenase	395	e-110
			CAA83234.1	cysteine dioxygenase type 1	395	e-110
			AAB58352.1	cysteine dioxygenase	395	e-110
			2024212A	Cys dioxygenase I	395	e-110
			AAH24241.1	cysteine dioxygenase, type I	395	e-110
			BAA12873.1	cysteine dioxygenase	392	e-109
NM_007820				cytochrome P450, subfamily IIIA, polypeptide 4; nifedipine oxidase; P450-III, steroid inducible; glucocorticoid-inducible P450; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3	729	0
NP_031846.1	Mm.30303	F:(C-D)+ 3.77	NP_059488.2	cytochrome P450 3A4 nifedipine oxidase (EC 1.14.14.-)	729	0
			A29815	nifedipine oxidase	729	0
			AAA35745.1	cytochrome P450 IIIA4	729	0
			AAF21034.1	cytochrome P450 polypeptide 4/	729	0
			AAG32290.1	Cytochrome P450 3A4 (Quinine 3-monooxygenase) (CYP11A4) (Nifedipine oxidase) (NF-25) (P450-PCN11)	729	0
			P08684	cytochrome P-450 (AA 1-503)	729	0
			CAA30944.1	cytochrome P450, family 3, subfamily A, polypeptide 5; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 5; aryl hydrocarbon hydroxylase; xenobiotic monooxygenase; microsomal monooxygenase; flavoprotein-linked monooxygenase; nifedipine oxidase	728	0
			NP_000768.1	Cytochrome P450 3A5 (CYP11A5) (P450-PCN3)	728	0
			P20815	cytochrome P450 3A5	728	0
			A34101	cytochrome P450 3A5	728	0

			AA02993.1	cytochrome P450 PON3		728	0
			AAH33862.1	cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 5		728	0
			AAA35744.1	cytochrome P-450 nifedipine oxidase		728	0
			AAF13598.1	cytochrome P450-3A4		726	0
			P05184	CP33_HUMAN Cytochrome P450 3A3 (CYP3A3) (HLp)		725	0
			A29410	cytochrome P450, glucocorticoid-inducible, hepatic - human		725	0
			AAA35742.1	glucocorticoid-inducible cytochrome P-450		725	0
			BA000001.1	cytochrome P-450		725	0
			2108280A	cytochrome P450-3A5		725	0
			AAA35747.1	cytochrome P450 nifedipine oxidase		718	0
		F:(C-D)+ 3.67 F:(C-H) +3.16					
AK012765			BAA12106.2	expressed ubiquitously with strong expression in brain		765	0
BAB28453.1	Mm.41557		NP_055681.2	KIAA0193 gene product		758	0
			AAH40492.1	Unknown (protein for MGC:33750)		758	0
			Q12765	Y193_HUMAN Hypothetical protein KIAA0193		642	0
			NP_612364.1	hypothetical protein BC002980		436 e-122	
			AAH17317.1	AAH17317 Unknown (protein for MGC:28622)		436 e-122	
			AAH10408.1	Unknown (protein for IMAGE:3945716)		435 e-122	
			AAH02980.1	AAH02980 Similar to KIAA0193 gene product		409 e-114	
			AAH20564.2	Similar to hypothetical protein MGC29406		395 e-107	
		F:(C-D)+ 3.6 F:(C-H) +3.48					
AJ133523			AAH35822.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 6 (GalNAc-T6)		1060	0
CAB55352.1	Mm.132399		BAC11118.1	unnamed protein product		1058	0

			AF183412.1 cytochrome P450 monooxygenase	348	8e-96
U98415	F:(C-D)+ 3.45				
AAC36522.1	F:(C-HI) +2.58	NULL	eukaryotic translation elongation factor 2; polypeptidyl-RNA translocase	444	e-125
			EF2 HUMAN Elongation factor 2 (EF-2)	444	e-125
			translation elongation factor eEF-2	444	e-125
			elongation factor 2	444	e-125
			human elongation factor 2	444	e-125
	F:(C-D)+ 3.41				
AF316872	F:(C-HI) +2.98		PTEN induced putative kinase 1; protein kinase BRPK	801	0
AAK28061.1		Mm.18539	AF316873.1 protein kinase BRPK	801	0
			PTEN induced putative kinase 1	801	0
			PTEN induced putative kinase 1	798	0
			Unknown (protein for IMAGE:3891886)	484	e-136
			unnamed protein product	408	e-113
	F:(C-D)+ 3.36				
NM_016661	F:(C-HI) +2.64		S-adenosylhomocysteine hydrolase; adenosylhomocysteinase	837	0
NP_057870.1		Mm.2573	SAHH_HUMAN Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)	837	0
			adenosylhomocysteinase (EC 3.3.1.1)	837	0
			S-adenosylhomocysteine hydrolase	837	0
			BK321BD2.1.2 (S-adenosylhomocysteine hydrolase (SAHH), isoform 2)	837	0
			S-adenosylhomocysteine hydrolase	837	0
			Similar to S-adenosylhomocysteine hydrolase	837	0

			AAA51881.1	S-adenosylhomocysteine hydrolase		835	0
				A Chain A, Structure Of Human Placental S-Adenosylhomocysteine Hydrolase: Determination Of A 30 Selenium Atom Substructure From Data At A Single Wavelength		799	0
			1A7A				
				B Chain B, Structure Of Human Placental S-Adenosylhomocysteine Hydrolase: Determination Of A 30 Selenium Atom Substructure From Data At A Single Wavelength		799	0
			1A7A				
			XP_065291.1	similar to Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)		619 e-177	
			CAC09529.1	bk3216D2.1.1 (S-adenosylhomocysteine hydrolase (SAH)), isoform 1		544 e-154	
			O43865	SAH2_HUMAN Putative adenosylhomocysteinase 2 (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)		440 e-123	
			AAC01980.1	S-adenosyl homocysteine hydrolase homolog		440 e-123	
			AAH07576.1	S-adenosylhomocysteine hydrolase-like 1		440 e-123	
			AAH10681.1	S-adenosylhomocysteine hydrolase-like 1		440 e-123	
			AAH16942.1	S-adenosylhomocysteine hydrolase-like 1		440 e-123	
			T08681	adenosylhomocysteinase (EC 3.3.1.1) DKFZp564A1523		440 e-123	
			CAB43223.1	hypothetical protein		440 e-123	
			NP_006612.2	S-adenosylhomocysteine hydrolase-like 1; S-adenosyl homocysteine hydrolase homolog		440 e-123	
			AAI26869.1	AF315687.1 S-adenosylhomocysteine hydrolase-like protein		440 e-123	
			NP_056143.1	KIAA0828 protein		438 e-122	
			Q98HN2	SAH3_HUMAN Putative adenosylhomocysteinase 3 (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)		438 e-122	
			AAH08349.1	Similar to S-adenosylhomocysteine hydrolase-like 1		438 e-122	
			AAH24325.1	KIAA0828 protein		438 e-122	
			BAA74851.1	KIAA0828 protein		438 e-122	

NM_013814 NP_038842.1	Mm.30249	F:(C-D)+ 3.35	NP_065207.2	polypeptide N-acetylgalactosaminyltransferase 1; UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1; GalNAc-T1; GalNAc transferase 1; protein-UDP acetyl-galactosaminyltransferase 1; UDP-GalNAc:polypeptide N-acetyl-galactosaminyltransferase 1	1118	0
			Q10472	PAGT_HUMAN Polypeptide N-acetyl-galactosaminyltransferase (Protein-UDP acetyl-galactosaminyltransferase) (UDP-GalNAc:polypeptide, N-acetyl-galactosaminyltransferase) (GalNAc-T1)	1118	0
			JC4223	polypeptide N-acetyl-galactosaminyltransferase (EC 2.4.1.41)	1118	0
			CAA59380.1	UDP-GalNAc:polypeptide N-acetyl-galactosaminyl transferase	1118	0
			Z119305A	UDP-GalNAc:polypeptide N-acetyl-galactosaminyltransferase	1116	0
			AAC50327.1	UDP-GalNAc:polypeptide N-acetyl-galactosaminyltransferase	1113	0
			BAC54545.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 13	968	0
			BAB67811.1	KIAA1918 protein	929	0
			NP_004472.1	polypeptide N-acetyl-galactosaminyltransferase 2; UDP-GalNAc transferase 2	451 e-126	
			I37405	polypeptide N-acetyl-galactosaminyltransferase (EC 2.4.1.41)	451 e-126	
			CAA59381.1	UDP-GalNAc:polypeptide N-acetyl-galactosaminyl transferase	451 e-126	
			AAH41120.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 2 (GalNAc-T2)	451 e-126	
			AAH136390.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 4 (GalNAc-T4)	427 e-119	
			AA045821.1	AC006017.1 N-acetyl-galactosaminyltransferase; similar to Q10473 (PID:gi709559)	426 e-119	
			AAH135822.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 6 (GalNAc-T6)	426 e-119	

						polypeptide N-acetylgalactosaminyltransferase 6; UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 6; protein-UDP acetylgalactosaminyltransferase 6; GalNAc transferase 6; GalNAc-T6	425 e-119	
						UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	425 e-119	
NM_023455 NP_075944.1		F:(C-D)+ 3.32 F:(C-H) +2.74 F:(H-D) +2.61				putative N-acetyltransferase Camello 2	223 4e-58	
						AF185571_1 putative N-acetyltransferase Camello 2	223 4e-58	
						N-acetyltransferase 8; kidney- and liver-specific gene; kidney- and liver-specific gene product	216 3e-56	
						AF187813_1 putative N-acetyltransferase CML1	216 3e-56	
						GLA	216 3e-56	
						kidney- and liver-specific gene	214 1e-55	
						hypothetical protein TSC501	214 1e-55	
						TSC501	214 1e-55	
NM_025279 NP_079555.1		F:(C-D)+ 3.32				heterogeneous nuclear ribonucleoprotein K isoform b; dC-stretch binding protein; transformation upregulated nuclear protein	635 0	
						ROK_HUMAN Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (dC-stretch binding protein) (CSBP) (Transformation upregulated nuclear protein) (TUNP)	635 0	
						heterogeneous nuclear ribonucleoprotein complex K; hnRNP K	635 0	
						heterogeneous nuclear ribonucleoprotein K	635 0	
						heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch binding protein; transformation upregulated nuclear protein	625 e-179	

			NP_002131.2	heterogeneous nuclear ribonucleoprotein K isoform α ; dC-stretch binding protein; transformation upregulated nuclear protein	625 e-179
			S43363	transformation upregulated nuclear protein	625 e-179
			AAH00355.1	heterogeneous nuclear ribonucleoprotein K	625 e-179
			CAA51267.1	transformation upregulated nuclear protein	622 e-178
			XP_002032.7	similar to heterogeneous nuclear ribonucleoprotein K [Rattus norvegicus]	176 4e-51
		F(C-D)+ 3.25			
NM_007611		F(C-HI) +3.1	NP_203124.1	caspase 7 isoform delta, large subunit; ICE-like apoptotic protease 3; apoptotic protease MCH-3; LICE2 alpha/beta/gamma	517 e-146
			AAC51152.1	LICE2 beta cysteine protease	517 e-146
			NP_001218.1	caspase 7 isoform alpha precursor; ICE-like apoptotic protease 3; apoptotic protease MCH-3; LICE2 alpha/beta/gamma	512 e-144
			NP_203125.1	caspase 7 isoform alpha, large subunit; ICE-like apoptotic protease 3; apoptotic protease MCH-3; LICE2 alpha/beta/gamma	512 e-144
			P55210	ICE7_HUMAN Caspase-7 precursor (ICE-like apoptotic protease 3) (ICE-LAP3)	512 e-144
			AAC50303.1	(Apoptotic protease Mch-3) (CMH-1)	512 e-144
			AAC50352.1	Mch3 isoform alpha	512 e-144
				CMH-1	512 e-144
			LICE2 gamma cysteine protease		512 e-144
			AAF21460.1	U67206 1 LICE2 alpha	512 e-144
			AAH15799.1	caspase 7, apoptosis-related cysteine protease	512 e-144
			AAC50346.1	ICE-LAP3	510 e-144
			1KMC	A Chain A, Crystal Structure Of The Caspase-7 XIAP-Bir2 Complex	508 e-143
			1KMC	B Chain B, Crystal Structure Of The Caspase-7 XIAP-Bir2 Complex	508 e-143
			1F1J	A Chain A, Crystal Structure Of Caspase-7 In Complex With Acetyl-Asp-Glu-Val-Asp-Gln	506 e-143
			1F1J	B Chain B, Crystal Structure Of Caspase-7 In Complex With Acetyl-Asp-Glu-Val-Asp-Gln	506 e-143

			1140	A Chain A, Crystal Structure Of The XIapCASPASE-7 Complex	489 e-138
			1140	B Chain B, Crystal Structure Of The XIapCASPASE-7 Complex	489 e-138
			1GQF	A Chain A, Crystal Structure Of Human Procaspase-7	477 e-134
			1GQF	B Chain B, Crystal Structure Of Human Procaspase-7	477 e-134
			1K86	A Chain A, Crystal Structure Of Caspase-7	474 e-133
			1K86	B Chain B, Crystal Structure Of Caspase-7	474 e-133
			1K88	A Chain A, Crystal Structure Of Procaspase-7	471 e-132
			1K88	B Chain B, Crystal Structure Of Procaspase-7	471 e-132
NM_009108					
NP_033134.1	MM3095	F:(C-D)+ 3.25	AA053550.1	AF478445_1 farnesoid-X-receptor beta splice variant 1	902
			AA053551.1	AF478446_1 farnesoid-X-receptor beta splice variant 2	896
			NP_005114.1	nuclear receptor subfamily 1, group H, member 4	857
			AA08107.1	farnesol receptor HRR-1	857
				NRH4 HUMAN Bile acid receptor (Farnesoid X-activated receptor) (Farnesol receptor HRR-1) (Retinoid X receptor-interacting protein 14) (RXR-interacting protein 14)	851
			Q06R11		851
			AA060271.1	AF384555_1 farnesol receptor	257
			NP_005684.1	nuclear receptor subfamily 1, group H, member 3; liver X receptor, alpha	257
			138975	nuclear orphan receptor LXR-alpha	257
			AA085856.1	nuclear orphan receptor LXR-alpha	257
			Q13133	NRH3 HUMAN Oxysterols receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan receptor LXR-alpha)	257
			AAH41172.1	Similar to nuclear receptor subfamily 1, group H, member 3	257
			AA056894.1	orphan receptor	243
				nuclear receptor subfamily 1, group H, member 2; ubiquitously-expressed nuclear receptor	243
			NP_009052.1		243

				P56055	NRH2_HUMAN Oxyterol receptor LXR-beta (Liver X receptor beta) (Nuclear orphan receptor LXR-beta) (Ubiquitously-expressed nuclear receptor) (Nuclear receptor NER)	243	6e-64
				JC4014	steroid hormone-nuclear receptor NER	243	6e-64
				AAA61783.1	Ner-1	243	6e-64
				AAH07790.1	nuclear receptor subfamily 1, group H, member 2	243	6e-64
NM_053069				NP_004840.1	APG5 autophagy 5-like; apoptosis specific protein	555	e-158
NP_444299.1	Mm.22264	F:(C-D)+ 3.22		Q9H1Y0	APG5_HUMAN Autophagy protein 5-like (APG5-like) (Apoptosis-specific protein)	555	e-158
				CAA72327.1	apoptosis specific protein	555	e-158
				AAH02699.1	APG5 (autophagy 5, S. cerevisiae)-like	555	e-158
				AAG44955.1	AF283841_1 apoptosis-related protein	389	e-108
NM_019744		F:(C-D)+ 3.19		NP_005428.1	nuclear receptor coactivator 4; RET-activating gene ELE1	928	0
NP_062718.1	Mm.28261	F:(C-HI) +2.56		Q13772	NCO4_HUMAN Nuclear receptor coactivator 4 (NCoA-4) (70 kDa androgen receptor coactivator) (70 kDa AR-activator) (Ret-activating protein ELE1)	928	0
				AAC37591.1	ORF	928	0
				CAB82390.1	hypothetical protein	928	0
				AAH01562.1	nuclear receptor coactivator 4	928	0
				S61532	RET oncogene fusion partner RFG	921	0
				CAA54673.1	Ret fused gene	921	0
				AAH12736.1	Similar to nuclear receptor coactivator 4	765	0
				AAH31551.1	ret/PTC3 chimeric protein	401	e-111
				CAA50536.1	ELE1	395	e-109
AJ276796							
CAC16403.1	Mm.21505	F:(C-D)+ 3.43		NP_001742.1	cysteine-tRNA ligase isoform b; cysteine transferase; cysteine-tRNA synthetase	1313	0

			P49589	SYC_HUMAN Cysteiny-IRNA synthetase (Cysteine-IRNA ligase) (CysRS)	1313	0
			AAG00578.1	AF288206_1 cytoplasmic cysteinyl-IRNA synthetase	1313	0
			AAH02880.1	cysteinyl-IRNA synthetase	1313	0
			NP_644802.1	cysteine-IRNA ligase isoform a; cysteine transase; cysteine-IRNA	1233	0
			AAG00579.1	AF288207_1 cysteinyl-IRNA synthetase	1233	0
			AAAT3901.1	cysteinyl-IRNA synthetase	1086	0
			NP_078813.1	hypothetical protein FLJ12118	241	3e-63
			BAB13978.1	unnamed protein product	241	3e-63
			AAH07220.1	hypothetical protein FLJ12118	240	6e-63
			BAB93499.1	OK/SW-CL10	221	4e-57
NM_010847			F:(C-D)+	MAX interacting protein 1 isoform a; MAX-interacting protein 1; MAX		
NP_034977.1	Mm.2154		NP_005953.2	dimerization protein 2	347	3e-95
			P50539	MX11_HUMAN MAX interacting protein 1 (MX11 protein)	346	7e-95
			AAAT7508.1	MX11 gene product	346	7e-95
			AAC50446.1	max interactor 1	346	9e-95
			2208335A	MX11 gene	346	9e-95
			AAH35128.1	Similar to MAX interacting protein 1	336	7e-92
			A45182	Max-associated protein Mx1	316	1e-87
			BAA09972.1	human Mx1 protein	317	4e-96
			NP_569157.1	MAX interacting protein 1 isoform b; MAX-interacting protein 1; MAX	288	2e-77
			AAH12907.1	dimerization protein 2	288	2e-77
				Similar to MAX-interacting protein 1		
			F:(C-D)+			
			3.03			
NM_013459			F:(H-D)	CFAD_HUMAN Complement factor D precursor (C3 convertase activator)	370	e-102
NP_038487.1	Mm.4407		P00746	(Properdin factor D) (Adipsin)	370	e-102
			CAC48304.1	adipsin/complement factor D precursor	358	4e-99

			DBHU	complement factor D (EC 3.4.21.46) precursor [validated]	352	5e-97
			1FDPIA	Chain A, Proenzyme Of Human Complement Factor D, Recombinant Profactor D	340	1e-93
			1FDPIB	Chain B, Proenzyme Of Human Complement Factor D, Recombinant Profactor D	340	1e-93
			1FDPIC	Chain C, Proenzyme Of Human Complement Factor D, Recombinant Profactor D	340	1e-93
			1FDPID	Chain D, Proenzyme Of Human Complement Factor D, Recombinant Profactor D	340	1e-93
			AAH34529	Unknown (protein for IMAGE:4780594)	340	1e-93
			1DST	Mutant Of Factor D With Enhanced Catalytic Activity	330	1e-90
			1DSUJA	Chain A, Human Factor D, Complement Activating Enzyme	329	3e-90
			1DSUJB	Chain B, Human Factor D, Complement Activating Enzyme	329	3e-90
			1DFPIA	Chain A, Factor D Inhibited By Diisopropyl Fluorophosphate	329	3e-90
			1DFPIB	Chain B, Factor D Inhibited By Diisopropyl Fluorophosphate	329	3e-90
			1BIO	Human Complement Factor D In Complex With Isotonic Anhydride Inhibitor	329	3e-90
			1HFD	Human Complement Factor D In A P21 Crystal Form	329	3e-90
			1DICJA	Chain A, Structure Of 3,4-Dichloroisocoumarin-Inhibited Factor D	329	3e-90
			NP_001919.1	adipsin/complement factor D precursor	324	1e-88
NM_019709				site-1 protease preproprotein; site-1 protease (subtilisin-like, sterol-regulated, cleaves sterol regulatory element binding proteins); subtilisin/kexin isozyme-1 preproprotein	2016	0
NP_062883.1	Mm.29791	F:(C-D)+ 3.03	NP_003782.1	MS1P_HUMAN Membrane-bound transcription factor site-1 protease precursor (Site-1 protease) (Subtilisin/kexin-isozyme-1) (SKL-1)	2016	0
			Q14703	KIAA00091	2016	0
			BAA07653.1	Similar to membrane-bound transcription factor protease, site 1	1049	0
			AAH26330.1	hypothetical protein DKFZp434A219.1	603	e-172
			T43492	hypothetical protein	603	e-172
			CAB63727.1	hypothetical protein	603	e-172

NM_007484 NP_031510.1	Mm.262	F:(C-D)+ 3.02
P08134	NP_786886.1	ras homolog gene family, member C; Aplysia RAS-related homolog 9(oncogene RHO H9); Aplysia ras-related homolog 9; RhoC; RAS homolog gene family, member C (oncogene RHO H9)
TVHJRC	P08134	RHO_C_HUMAN Transforming protein RhoC (H9)
CAV29969.1	AAAC33179.1	GTP-binding protein rhoC
AAH07245.1	AAH09177.1	rhoC coding region (AA 1-193)
AAH09177.1	AAM21119.1	GTPase
NP_001655.1	NP_001655.1	ras homolog gene family, member C
P06749	P06749	ras homolog gene family, member C
TVHU12	CAV28690.1	AF-498972_1 small GTP binding protein RhoC
CAV28690.1	CAV28690.1	ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho12; RhoA; Ras homolog gene family, member A (oncogene RHO H12)
AAH01360.1	AAH01360.1	RHOA_HUMAN Transforming protein RhoA (H12)
AAH05976.1	AAH05976.1	GTP-binding protein rhoA
AAM21117.1	AAM21117.1	ORF (AA 1-193)
1LB1	1LB1	GTP-binding protein
1LB1	1LB1	ras homolog gene family, member A
1LB1	1LB1	ras homolog gene family, member A
1LB1	1LB1	AF-498970_1 small GTP binding protein RhoA
1LB1	1LB1	B Chain B, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In Complex With Rhoa
1LB1	1LB1	D Chain D, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In Complex With Rhoa
1LB1	1LB1	F Chain F, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In Complex With Rhoa
1LB1	1LB1	H Chain H, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In Complex With Rhoa
1FTN	1FTN	Crystal Structure Of The Human RhoGDP COMPLEX

			11VH	C Chain C, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	739	0
			11VH	D Chain D, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	739	0
			NP_000008.1	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain precursor	257	3e-68
			P18219	ACDS_HUMAN Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor (SCAD) (Butyryl-CoA dehydrogenase)	257	3e-68
			A30605	acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, short-chain-specific	257	3e-68
			AAA60307.1	short chain acyl-CoA dehydrogenase precursor (EC 1.3.99.2)	257	3e-68
			CAB02492.1	acyl-CoA dehydrogenase	257	3e-68
			AAD00552.1	short chain acyl CoA dehydrogenase	257	3e-68
			1704375A	short chain acyl-CoA dehydrogenase	257	3e-68
			AAH25983.1	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	254	1e-67
			NP_001600.1	acyl-Coenzyme A dehydrogenase, short/branched chain precursor	245	8e-65
			P45954	ACDB_HUMAN Acyl-CoA dehydrogenase, short/branched chain specific, mitochondrial precursor (SBCAD) (2-methyl branched chain acyl-CoA dehydrogenase) (2-MEBCAD) (2-methylbutyryl-coenzyme A dehydrogenase)	245	8e-65
			A55680	acyl-CoA dehydrogenase (EC 1.3.99.-) short/branched chain specific precursor	245	8e-65
			AAA74424.1	acyl-CoA dehydrogenase	245	8e-65
			AAH97921.1	short/branched chain acyl-CoA dehydrogenase	245	8e-65
			AAH13756.1	Unknown (protein for MGC:21286	245	8e-65
			CAD38535.1	hypothetical protein.	245	1e-64
			1EGD	A Chain A, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	238	2e-62
			1EGD	B Chain B, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	238	2e-62
			1EGD	C Chain C, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	238	2e-62

AF320996			1EGD	D Chain D, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	238	2e-62
AAK73808.1	Mm.14569	F:(C-D)+ 2.99	1EGC	A Chain A, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase Complexed With Octanoyl-CoA	238	2e-62
			1EGC	B Chain B, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase Complexed With Octanoyl-CoA	238	2e-62
			1EGC	C Chain C, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase Complexed With Octanoyl-CoA	238	2e-62
			1EGC	D Chain D, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase Complexed With Octanoyl-CoA	238	2e-62
			AAF63628.1	medium-chain acyl-CoA dehydrogenase	236	6e-62
			NP_057712.2	WW domain-containing adapter with a coiled-coil region isoform 1	1044	0
			NP_567822.1	WW domain-containing adapter with a coiled-coil region isoform 2	951	0
			BAB71029.1	unnamed protein product	949	0
			AAH04258.1	hypothetical protein PRO1741	938	0
			CAC16000.1	bA48B24.1 (A novel protein containing a formin binding protein (FBP28) domain)	861	0
			CAD28517.1	hypothetical protein	588	e-168
			BAB47473.1	KIAA1844 protein	533	e-151
			NP_567823.1	WW domain-containing adapter with a coiled-coil region isoform 3	521	e-147
			AAH10356.1	hypothetical protein MGC10753	350	5e-96
			NP_004069.1	cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain protein	326	3e-99
			P21291	CYSR_HUMAN Cysteine-rich protein 1 (CRP1) (CRP)	326	3e-99
			S12858	cysteine-rich protein	326	3e-99
			AAA58431.1	cysteine-rich protein	326	3e-99
			AAA35720.1	cysteine-rich protein	326	3e-99
			AAH32493.1	cysteine and glycine-rich protein 1	326	3e-99
NM_007791			F:(C-D)+ 2.93			
NP_031817.1	Mm.196484					

			Q9UC90	PGN_HUMAN Paraplegin (Spastic paraplegia protein 7)	489 e-138	
			AAD28099.1	paraplegin	489 e-138	
			AAK57555.1	ATP-dependent metalloprotease Fish1 homolog	346 1e-94	
			NP_647473.1	YME1-like 1 isoform 1; ATP-dependent metalloprotease Fish1 homolog	346 1e-94	
			NP_055078.1	YME1-like 1 isoform 3; ATP-dependent metalloprotease Fish1 homolog	346 1e-94	
			CAB51858.1	ATP-dependent metalloprotease YME1L	346 1e-94	
			AAH24032.1	YME1-like 1 (S. cerevisiae)	346 1e-94	
			AAH23507	YME1-like 1 (S. cerevisiae)	346 1e-94	
			AAD20962.1	Fish1 homolog	345 2e-94	
			CAB99462.1	putative ATPases	344 3e-94	
			NP_647474.1	YME1-like 1 isoform 2; ATP-dependent metalloprotease Fish1 homolog	341 2e-93	
			AAH07795.1	similar to YME1-like 1 (S. cerevisiae)	341 2e-93	
AK010065 BAB26679.1				isocitrate dehydrogenase 3 (NAD+) alpha precursor; isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial; NAD(+)-specific IDH; NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor; isocitrate dehydrogenase (NAD+) alpha chain precursor; H-IDH alpha; isocitric dehydrogenase [Homo sapiens]	720 0	
		F:(C-D)+ 2.9	NP_005521.1	IDHA_HUMAN isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor	720 0	
			P50213	isocitrate dehydrogenase (NAD) (EC 1.1.1.41) alpha chain precursor	720 0	
			S55282	NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor	720 0	
			AAA85639.1	isocitrate dehydrogenase 3 (NAD+) alpha	720 0	
			AAH21967.1	hypothetical protein	571 e-162	
			CAC09449.1	isocitrate dehydrogenase 3, beta subunit isoform b precursor; isocitric dehydrogenase; NAD(+)-specific isocitrate dehydrogenase beta precursor; NAD(+)-specific isocitrate dehydrogenase b subunit; NAD(+)-specific IDH; isocitrate dehydrogenase, NAD(+)-specific, mitochondrial, beta subunit	283 4e-76	
			NP_777280.1	dJ686C3.1.1 (isocitrate dehydrogenase 3 (NAD+) beta (isoform A)	283 4e-76	
			CAC01443.1	NAD(+)-specific isocitrate dehydrogenase beta subunit isoform A	283 4e-76	
			AAD09339.1			

				isocitrate dehydrogenase 3, beta subunit isoform a precursor; isocitric dehydrogenase; NAD(+)-specific isocitrate dehydrogenase beta precursor; NAD(+)-specific isocitrate dehydrogenase b subunit; NAD(+)-specific ICDH; isocitrate dehydrogenase, NAD(+)-specific, mitochondrial, beta subunit	276	5e-74
			NP_008830.2	Similar to isocitrate dehydrogenase 3 (NAD+) beta	276	5e-74
			AAH01980.1	dJ886C3.1.2 (isocitrate dehydrogenase 3 (NAD+) beta (isoform B))	276	5e-74
			CAC01442.2	IDHb_HUMAN isocitrate dehydrogenase [NAD] subunit beta, mitochondrial precursor (isocitric dehydrogenase) (NAD(+)-specific ICDH)	278	5e-74
			O43837	NAD(+)-specific isocitrate dehydrogenase beta precursor	276	5e-74
			AAE94295.1	isocitrate dehydrogenase (NAD) (EC 1.1.1.41) beta chain isoform B	276	5e-74
			T13147	NAD(+)-specific isocitrate dehydrogenase beta subunit isoform B	276	5e-74
			AAD08340.1	isocitrate dehydrogenase 3 (NAD+) gamma isoform a precursor; isocitric dehydrogenase; isocitrate dehydrogenase, NAD(+)-specific, mitochondrial, gamma subunit; IDH-gamma; NAD(+)-specific ICDH; NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor	275	2e-73
			NP_004126.1	IDHG_HUMAN isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial precursor (isocitric dehydrogenase) (NAD(+)-specific ICDH)	275	2e-73
			P51553	NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor	275	2e-73
			CAA93143.1	NAD(H)-specific isocitrate dehydrogenase gamma-subunit precursor	275	2e-73
			CAA92214.1	NAD(+)-specific isocitrate dehydrogenase gamma subunit precursor	275	2e-73
			AAD08357.1	isocitrate dehydrogenase 3 (NAD+) gamma	275	2e-73
			AAH00933.1	isocitrate dehydrogenase 3 (NAD+) gamma	272	8e-73
			AAH01902.1	isocitrate dehydrogenase 3 (NAD+) gamma isoform b precursor; isocitric dehydrogenase; isocitrate dehydrogenase, NAD(+)-specific, mitochondrial, gamma subunit; IDH-gamma; NAD(+)-specific ICDH; NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor	261	2e-69
NM_025876				CDK5 regulatory subunit associated protein 1 isoform a, CDK5 activator-binding protein C42-like; chromosome 20 open reading frame 34	1030	0
NP_080152.1	Mm.74138	F:(C-D)+ 2.88	NP_057492.2	unamed protein product	1030	0
			BAB14760.1	(CGI-05 protein (LOC51654) similar to rat CDK5 activator-binding protein)	987	0
			CAC15883.2			

				AAH17034.1	AAH17034 lysophospholipase II	305	5e-83
				AAH17193.1	AAH17193 lysophospholipase II	305	5e-83
				XP_212610.1	similar to lysophospholipase II; acyl-protein thioesterase	285	5e-77
				XP_208353.1	similar to lysophospholipase II; acyl-protein thioesterase	285	5e-77
				XP_208353.1	du570F3.6 (novel protein similar to lysophospholipase II (LYPLA2))	285e +02	5e-77
NM_019649				AAH04865.1	AAH04865 cleft lip and palate associated transmembrane protein 1	835	0
NP_062623.1				NP_001285.1	left lip and palate associated transmembrane protein 1	835	0
				AAC97420.1	cleft lip and palate transmembrane protein 1	835	0
				AAC98151.1	cleft lip and palate transmembrane protein 1	835	0
				AAH12359.1	AAH12359 Similar to cleft lip and palate associated transmembrane protein 1	835	0
				NP_110409.2	cisplatin resistance related protein CRR9p	164	1e-80
				BAB55030.1	unnamed protein product	164	1e-80
				AAH25305.1	cisplatin resistance related protein CRR9p	164	1e-80
				JC7599	cisplatin(CDDP) resistance related protein CRR	164	1e-80
				BAB20063.1	cisplatin resistance related protein CRR9p	164	1e-80
				AAH16399.1	AAH16399 Unknown (protein for IMAGE:3864810)	164	4e-68
NM_023854				AAH30148.1	zinc finger protein 289, ID1 regulated	849	0
NP_076343.1				NP_115765.1	zinc finger protein 289, ID1 regulated; likely ortholog of mouse ZFP289	847	0
				BAB55144.1	unnamed protein product	847	0
				CAD39004.1	hypothetical protein	844	0
				NP_055385.2	ADP-ribosylation factor GTPase activating protein 3; ADP-ribosylation factor GTPase activating protein 1	447	e-125
				AAH05122.1	AAH05122 ADP-ribosylation factor GTPase activating protein 1	447	e-125
				Q9NP61	ARG3_HUMAN ADP-ribosylation factor GTPase-activating protein 3	446	e-125

			CAB76901.1	hypothetical protein	446 e-125
			AAF40310.1	AF111847_1 ARFGAP1 protein	446 e-126
			T46305	hypothetical protein DKFZp434D1411.1 - human (fragment)	374 e-103
			CAB70834.1	hypothetical protein	374 e-103
		F:(C-D)+ 2.83 F:(C-HI) +2.5			
NM_009825			AAH36298.1	Unknown (protein for IMAGE:4748644)	731 0
NP_033955.1	Mm.22708			serine (or cysteine) proteinase inhibitor, clade H, member 1; collagen-binding protein 1; gp46; colligin-1; collagen-binding protein 2; colligin-2; heat shock protein 47	726 0
			NP_004344.1	HS47_HUMAN 47 kDa heat shock protein precursor (Collagen-binding protein 1)	726 0
			P29043	heat shock protein Hsp47 precursor	726 0
			S20608	colligin	726 0
			CAA43795.1	CBP2_HUMAN Collagen-binding protein 2 precursor (Colligin 2) (Rheumatoid arthritis related antigen RA-A47)	723 0
			P50454	rheumatoid arthritis related antigen RA-A47	723 0
			BAA96788.1	rheumatoid arthritis related antigen RA-A47	723 0
			BAA96789.1	rheumatoid arthritis related antigen RA-A47	723 0
			AAH14623.1	AAH14623 Unknown (protein for MGC:4258)	723 0
				serine (or cysteine) proteinase inhibitor, clade H, member 1; collagen-binding protein 1; gp46; colligin-1; collagen-binding protein 2; colligin-2; heat shock protein 47	
			NP_001226.1	colligin-2	719 0
			I52968	collagen binding protein 2	719 0
			BAA11829.1	rheumatoid arthritis-related antigen RA-A47	347 5e-95
			BAA96790.1	rheumatoid arthritis related antigen RA-A47	347 5e-95
			BAA96791.1	ancient ubiquitous 46 kDa protein AUP1	549 e-156
NM_007517					
NP_031543.1	Mm.2146	F:(C-D)+ 2.82			

	AAF66945.1	AF165515_1 ancient ubiquitous protein 1 precursor		549 e-156
	AAH33846.1	ancient ubiquitous protein 1		549 e-156
	AAD43010.1	AUP1 homolog		548 e-156
	BAB14753.1	unnamed protein product		492 e-139
	NP_036235.1	ancient ubiquitous protein 1		431 e-120
	Q9Y679	AUP1_HUMAN Ancient ubiquitous protein 1 precursor		431 e-120
	AAD43018.1	ancient ubiquitous protein AUP1 isoform		431 e-120
		v-akt murine thymoma viral oncogene homolog 2; Murine thymoma viral (v-akt) homolog-2; rac protein kinase beta		966
	NP_001617.1	AKT2_HUMAN RAC-beta serine/threonine protein kinase (RAC-PK-beta) (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta)		966
	P31751	protein kinase (EC 2.7.1.37) akt2		966
	A46288	protein serine/threonine kinase		966
	AAA58364.1	rac protein kinase-beta		959
	AAA36585.1	AAH00479 v-akt murine thymoma viral oncogene homolog 1		823
	AAH00479.1	serine/threonine protein kinase; Murine thymoma viral (v-akt) oncogene homolog-1		823
	NP_005154.1	KRAC_HUMAN RAC-alpha serine/threonine kinase (RAC-PK-alpha) (Protein kinase B) (PKB) (C-AKT)		823
	P31749	protein kinase (EC 2.7.1.37) akt1 [validated]		823
	A39360	rac protein kinase-alpha		823
	AAA36539.1	AKT1		823
	AAL55732.1	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma); protein kinase B gamma		770
	NP_005456.1	AKT3_HUMAN RAC-gamma serine/threonine protein kinase (RAC-PK-gamma) (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (STK-2)		770
	Q9Y243	protein kinase (EC 2.7.1.37) akt3 long splice form [similarity]		770
	A59380	AF135794_1 AKT3 protein kinase		770
	AAD24196.1			770

					AF124141_1 protein kinase B gamma	770	0
					Akt-3 protein	770	0
					AF085234_1 STK-2	770	0
					protein kinase (EC 2.7.1.37) akt3 short splice form	743	0
					hypothetical protein	743	0
					CAB55977.1	743	0
					AAF91073.1	743	0
					human protein kinase B	700	0
					CAA43372.1		
					106K	672	0
					106L	647	0
		F:(C-D)+ 2.81 F:(C-H) +2.87					
AK016546		Mm.202749			dipeptidyl peptidase 8 isoform 1; dipeptidyl peptidase 8	1694	0
BAB30295.2					AF221634_1 dipeptidyl peptidase 8	1694	0
					dipeptidyl peptidase IV-related protein-1	1694	0
					similar to dipeptidyl peptidase 8	1693	0
					Similar to dipeptidyl peptidase 8	1589	0
					dipeptidyl peptidase 8 isoform 2; dipeptidyl peptidase 8	1271	0
					unnamed protein product	1205	0
					dipeptidyl peptidase 9; dipeptidyl peptidase 9; dipeptidyl peptidase IV-related protein-2	1068	0
					AF452102_1 dipeptidyl peptidase-like protein 9	1068	0
					dipeptidyl peptidase 9	1068	0
					dipeptidyl peptidase IV-related protein-2	1068	0
					unnamed protein product	892	0
					hypothetical protein	804	0

			AAC29768.1	AF221638_1 dipeptidyl peptidase 8	670	0
			AAC33801.1	R26984_1	613	e-175
AK010356		F:(C-D)+ 2.81	NP_071330.1	differentially expressed in FDCP 6 homolog; differentially expressed in FDCP (mouse homolog) 6	243	2e-64
BAB28876.1	Mm.60230		CAC08450.1	Def-6 protein	243	2e-64
			AAH07702.1	AAH07702 Similar to differentially expressed in FDCP (mouse homolog) 6	243	2e-64
		F:(C-D)+ 2.8 F:(C-HI) +2.71	NP_060817.1	chromosome 20 open reading frame 29	234	1e-74
AK002807			Q9NUS5	CT29_HUMAN Protein C20orf29	234	1e-74
BAC29007.1	Mm.2937		BAA92045.1	unnamed protein product	234	1e-74
			CAC17552.1	dJ1009E24.7.1	234	1e-74
			AAH43344.1	chromosome 20 open reading frame 29	234	1e-74
			NP_006511.1	t-complex-associated-testis-expressed 1-like	224	3e-59
NM_025975		F:(C-D)+ 2.8	P51808	TCTL_HUMAN T-complex associated-testis-expressed 1-like (Protein 91/23)	224	3e-59
NP_060251.2	Mm.29150		i38410	RP3 candidate gene	224	3e-59
			AA57444.1	RP3 candidate gene	224	3e-59
			AAH00968.1	AAH00968 t-complex-associated-testis-expressed 1-like	224	3e-59
			NP_036476.1	neurotensin receptor 2; neurotensin receptor, type 2; levocabastine-sensitive neurotensin receptor	224	3e-59
NM_008747		F:(C-D)+ 2.8	O95665	NTR2_HUMAN Neurotensin receptor type 2 (NT-R-2) (Levocabastine-sensitive neurotensin receptor) (NTR2 receptor)	526	e-149
NP_032773.1	Mm.5153		CAA71233.1	neurotensin receptor 2	526	e-149
			AAH22501.1	neurotensin receptor 2	524	e-148
			AAH37776.1	Similar to neurotensin receptor 2	463	e-130
			NP_002522.1	neurotensin receptor 1	263	6e-70

			P30689	NTR1_HUMAN Neurotensin receptor type 1 (NT-R-1) (High-affinity levocabastine-insensitive neurotensin receptor) (NTRH)	263	6e-70
			S29506	neurotensin receptor	263	6e-70
			CAA49875.1	neurotensin receptor	263	6e-70
			1907158A	neurotensin receptor	263	6e-70
NM_025459			BAB15241.1	unnamed protein product	572	e-183
NP_079735.1	Mm.25311	F:(C-D)+ 2.76	NP_061873.2	hypothetical protein FLJ20152	571	e-182
			BAB15034.1	unnamed protein product	571	e-182
			BAA90982.1	unnamed protein product	204	2e-52
			AAH30517.1	hypothetical protein FLJ20152	204	2e-52
			BAB15252.1	unnamed protein product	202	7e-52
NM_016774	Mm.103838	F:(C-D)+ 2.74	P06576	ATPB_HUMAN ATP synthase beta chain, mitochondrial precursor	893	0
NP_068054.1			A33370	H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain precursor, mitochondrial	893	0
			AAA51809.1	ATP synthase beta subunit precursor	893	0
			AAH16512.1	AAH16512 Similar to ATP synthase, H+-transporting, mitochondrial F1 complex, beta polypeptide	893	0
			NP_001677.1	ATP synthase, H+-transporting, mitochondrial F1 complex, beta polypeptide; ATP synthase, H+-transporting, mitochondria F1 complex, beta	890	0
			CAA27246.1	put. F1-beta precursor	890	0
			BAA00016.1	F1 beta subunit	890	0
			I202298A	ATPase beta, F1	890	0
			AAA51808.1	ATP synthase beta subunit	879	0

			CAA29095.1	beta-subunit (AA 1-312)	597 e-170
				ATPase, H ⁺ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1; ATPase, H ⁺ transporting, lysosomal, beta polypeptide, 58kD; vacuolar proton pump, subunit 3; vacuolar ATP synthase subunit B, kidney isoform; V-ATPase B1 subunit; endomembrane proton pump 58 kDa subunit; H(+)-transporting two-sector ATPase, 58kD subunit; H(+)-ATPase beta 1 subunit; ATPase, H ⁺ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1 (Renal tubular acidosis with deafness)	100 5e-21
AK010325 NP_542123.1	F:(C-D)+ 2.72 F:(C-H) +2.78 Mm.5885		NP_001683.2	transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2	1176 0
			Q99805	T9S2_HUMAN Transmembrane 9 superfamily protein member 2 precursor (p76)	1176 0
			AA838973.1	p76	1176 0
			NP_055557.1	K1AA0255 gene product	470 e-136
			Q92544	T9S4_HUMAN Transmembrane 9 superfamily protein member 4	470 e-136
			BAA13385.1	Similar to S.cerevisiae EMP70 protein precursor (S25110)	470 e-136
			CAB75607.2	dJ836N17.2 (K1AA0255 protein)	470 e-136
			AAH21107.1	AAH21107 K1AA0255 gene product	470 e-136
			AAH22850.1	K1AA0255 gene product	470 e-136
			AAF98159.1	AF289150_1 transmembrane protein TM9SF3	256 2e-69
			Q9HD45	T9S3_HUMAN Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-iso)	256 2e-69
			AAF21983.1	SM-11044 binding protein	256 2e-69
			BAB55388.1	unnamed protein product	256 3e-69
			BAA91362.1	unnamed protein product	256 1e-68

				AAH20959.1	AAH20959 Unknown (protein for MGC:8842)	254	1e-68
				BAC11232.1	unnamed protein product	249	3e-67
				NP_006396.2	transmembrane 9 superfamily member 1; multispreading membrane protein (70KD); transmembrane protein 9 superfamily member 1	251	4e-66
				AAH10856.1	AAH10856 Unknown (protein for MGC:9160)	251	4e-66
				CAD61879.1	unnamed protein product	251	4e-66
				F:(C-D)+ 2.72 F:(C-HI) +2.64			
NM_019973				AAK07692.1	NREBP	2386	0
NP_064357.1	Min.46401			NP_003094.3	SON DNA-binding protein isoform G; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in Saccharomyces 1	2384	0
				P18583	SON_HUMAN SON protein (SON3) (Negative regulatory element-binding protein) (NRE-binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1) (BASS1) (Protein C21orf90)	2373	0
				AAL34502.1	AF380184_1 SON DNA binding protein isoform F	2373	0
				AAL34498.1	AF380180_1 SON DNA binding protein isoform B	2373	0
				AAL34499.1	AF380181_1 SON DNA binding protein isoform C	2373	0
				AAL34501.1	AF380183_1 SON DNA binding protein isoform E	2373	0
				NP_620304.1	SON DNA-binding protein isoform C; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in Saccharomyces 1	2371	0
				NP_620305.1	SON DNA-binding protein isoform F; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in Saccharomyces 1	2371	0
				NP_115571.1	SON DNA-binding protein isoform B; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in Saccharomyces 1	2371	0

AK005989 BAB24354.1			NP_478063.2	SON DNA-binding protein isoform E: NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Box antagonist selected in <i>Saccharomyces</i> 1	2371	0
	F:(C-D)+ 2.72	Mm.182959	NP_005733.1	protein disulfide isomerase-related protein	714	0
			Q15084	PDA6_HUMAN Protein disulfide isomerase A6 precursor (Protein disulfide isomerase P5)	714	0
			IC4369	P5 protein precursor	714	
			BAA08450.1	human P5	714	0
			AAH01312.1	AAH01312 protein disulfide isomerase-related protein	714	0
			AAB50217.1	protein disulfide isomerase-related protein 5	681	0
AK004564 BAB23375.1	F:(C-D)+ 2.71	Mm.46346	BAC03493.1	unnamed protein product	1190	0
			BAC05316.1	unnamed protein product	675	0
			AAH32598.1	Similar to RIKEN cDNA 1200003G01 gene	572	e-162
			XP_113607.1	similar to CG12547 gene product [<i>Drosophila melanogaster</i>]	200	1e-50
Y00769 CAA68738.1	F:(C-D)+ 2.71	Mm.4712	NP_002202.2	integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fibronectin receptor beta subunit	1471	0
			NP_596867.1	integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fibronectin receptor beta subunit	1471	0
			AAH20057.1	AAH20057 Unknown (protein for MGC:17220)	1471	0
			P05556	ITB1_HUMAN Integrin beta-1 precursor (Fibronectin receptor beta subunit) (CD29 antigen) (Integrin VLA-4 beta subunit)	1467	0
			B27079	fibronectin receptor beta chain precursor	1467	0
			CAA30790.1	integrin beta 1 subunit precursor	1467	0
			NP_391988.1	integrin beta 1 isoform 1D precursor; integrin VLA-4 beta subunit; fibronectin receptor beta subunit	1450	0

			NP_388647.1	integrin beta 1 isoform 1B precursor; integrin VLA-4 beta subunit; fibronectin receptor beta subunit	1428	0
			NP_391987.1	integrin beta 1 isoform 1C-1 precursor; integrin VLA-4 beta subunit; fibronectin receptor beta subunit	1428	0
			NP_391989.1	integrin beta 1 isoform 1C-2 precursor; integrin VLA-4 beta subunit; fibronectin receptor beta subunit	1428	0
			CAB90553.1	cell surface adhesion glycoprotein (LFA-1/CR3/p150,959 beta subunit precursor)	655	0
			NP_000202.1	integrin beta chain, beta 2 precursor; Integrin, beta-2 (antigen CD18 (p95), lymphocyte function-associated; cell surface adhesion glycoprotein (LFA-1/CR3/p150,959 beta subunit precursor)	653	0
			P05107	ITB2_HUMAN Integrin beta-2 precursor (Cell surface adhesion glycoproteins LFA-1/CR3/p150,95 beta-subunit) (CD18) (Complement receptor C3 beta-subunit)	653	0
			IJHULM	leukocyte adhesion protein beta chain (CD18) precursor	653	0
			AAA59490.1	leukocyte adhesion protein beta-subunit precursor	653	0
			CAA45427.1	integrin beta-2 subunit	653	0
			AAH05861.1	AAH05861 integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	653	0
			CA08266.1	precursor polypeptide (AA-14 to 747)	652	0
			NP_000880.1	integrin, beta 7	642	0
			P26010	ITB7_HUMAN Integrin beta-7 precursor	642	0
			A40526	integrin beta-7 chain precursor	642	0
			AAA59184.1	integrin beta-7 subunit	642	0
			AAA59185.1	integrin beta-7 subunit	642	0

				AAB21332.1	integrin beta 7 subunit	642	0
				AAB23688.1	integrin beta 7 subunit	642	0
				AAA36118.1	integrin beta 7 subunit	642	0
				AAH15916.1	AAH15916 integrin, beta 7	642	0
		F(C-D) ⁺ 2.7			catenin (cadherin-associated protein), beta 1, 88kDa; catenin (cadherin-associated protein), beta 1 (88kDa)		
NM_007814 NP_031640.1	1Mm.3476	F(C-HI) +2.75		NP_001895.1	protein, beta 1 (88kDa)	1523	0
				P35222	CTNB_HUMAN Beta-catenin (PRO2286)	1523	0
				A38973	beta-catenin	1523	0
				CAA79497.1	beta catenin	1523	0
				CAA61107.1	beta-catenin	1523	0
				2208332A	beta-catenin	1523	0
				1JPW	A Chain A, Crystal Structure Of A Human Tcf-4 BETA-Catenin Complex	1026	0
				1JPW	B Chain B, Crystal Structure Of A Human Tcf-4 BETA-Catenin Complex	1026	0
				1JPW	C Chain C, Crystal Structure Of A Human Tcf-4 BETA-Catenin Complex	1026	0
				1G3J	A Chain A, Crystal Structure Of The Xtc3-CtdBETA-Catenin Armadillo Repeat Complex	1014	0
				1G3J	C Chain C, Crystal Structure Of The Xtc3-CtdBETA-Catenin Armadillo Repeat Complex	1014	0
				1UDH	A Chain A, Crystal Structure Of Beta-Catenin And Hicf-4 catenin beta 1	1007	0
				BAB93475.1	catenin beta 1	984	0
				1LUJ	A Chain A, Crystal Structure Of The Beta-Catenin/CAT COMPLEX	979	0
				AAH00441.1	AAH00441 junction plakoglobin	929	0
				AAH11865.1	AAH11865 junction plakoglobin	929	0
				NP_002221.1	junction plakoglobin isoform 1; gamma-catenin	929	0

	NM_068831.1	junction plakoglobin isoform 1; gamma-catenin	929	0
	CAG97522.1	plakoglobin	929	0
	AAG16727.1	plakoglobin	929	0
	P14923	PLAK_HUMAN Junction plakoglobin (Desmoplakin III)	913	0
	A32905	plakoglobin, desmosomal	913	0
	AAA64895.1	Plakoglobin	912	0
	CAA27300.1	put. c-fms precursor colony stimulating factor 1 receptor precursor; FMS proto-oncogene; CD115 antigen; macrophage colony stimulating factor I receptor; similar to mouse Friend murine leukemia virus integration site 2	1392	0
	NP_005202.2	KFMs HUMAN Macrophage colony stimulating factor I receptor precursor (CSF-1-R) (Fms proto-oncogene) (c-fms) (CD115 antigen)	1392	0
	P07333	macrophage colony-stimulating factor 1 receptor precursor	1392	0
	TVHUMD	[CSF-1 receptor]	1392	0
	AAB51696.1	gene c-fms	1392	0
	I204266A	Colony stimulating factor 1 receptor, precursor	1399	0
	AAH47521.1	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog precursor	637	0
	NP_000213.1	KIT_HUMAN Mast/stem cell growth factor receptor precursor (SCFR) (Proto-oncogenic tyrosine-protein kinase Kit) (c-kit) (CD117 antigen)	637	0
	P10721	protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor	637	0
	TVHUKT	protein p145-ckit (AA 1 - 976)	637	0
	CAAA29548.1	mast/stem cell growth factor receptor	637	0
	CAAA49159.1	KIT protein	637	0
	AAC50968.1		637	0

				AAC50969.1	KIT protein		634	0
				NP_006197.1	platelet-derived growth factor receptor alpha precursor		479	e-135
				P16234	PGDS_HUMAN Alpha platelet-derived growth factor receptor precursor (PDGF-R-alpha) (CD140a antigen)		479	e-135
				PFHUGA	platelet-derived growth factor receptor alpha precursor		479	e-135
				AAA60048.1	platelet-derived growth factor A receptor		479	e-135
				AAA96715.1	platelet-derived growth factor receptor A chain		479	e-135
				BAA08742.1	alpha-platelet-derived growth factor receptor		479	e-135
					platelet-derived growth factor receptor beta precursor; beta			
				NP_002600.1	platelet-derived growth factor receptor		473	e-133
				P09619	PGDR_HUMAN Beta platelet-derived growth factor receptor precursor (PDGF-R-beta) (CD140b antigen)		473	e-133
				PFHUGB	platelet-derived growth factor receptor beta precursor		473	e-133
				AAA60049.1	platelet-derived growth factor receptor		473	e-133
				AAH32224.1	platelet-derived growth factor receptor, beta polypeptide		473	e-133
				AAA36427.1	platelet-derived growth factor receptor		473	e-133
				CAA81393.1	FLT3 receptor tyrosine kinase		419	e-116
NM_007415					PPOL_HUMAN Poly [ADP-ribose] polymerase-1 (PARP-1) (ADPRT)		1736	0
NP_031441.2	Mm.9248	F:(C-D)+ 2.7		P09874	(NAD(+)-ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1)		1736	0
				A29725	NAD ADP-ribosyltransferase (EC 2.4.2.30), nuclear		1736	0
				AAA51663.1	NAD+ ADP-ribosyltransferase			
					AF524947_1 ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase		1736	0
				AAM75364.1	poly(ADP-ribose) polymerase		1735	0
				AA60137.1	poly(ADP-ribose) polymerase		1734	0
				AAH37545.1	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)			

				AA859447.1	poly(ADP-ribose) synthetase	1731	0
				NP_001609.1	poly(ADP-ribose) transferase; ADP-ribose transferase NAD(+); poly(ADP-ribose) synthetase	1722	0
				AAA80155.1	poly(ADP-ribose) polymerase	1722	0
				AAA51599.1	poly(ADP-ribose) polymerase	1004	0
				XP_062787.1	similar to Poly(ADP-ribose) polymerase-1 (PARP-1) (ADPRT) (NAD(+)) ADP-ribose transferase-1) (Poly(ADP-ribose) synthetase-1)	521	e-147
				CAB41505.2	poly(ADP-ribose) polymerase-2	367	e-101
				AF479321_1	ADP-ribose transferase (NAD+; poly(ADP-ribose) polymerase) like	367	e-101
				AA177437.1	P202_HUMAN Poly(ADP-ribose) polymerase-2 (PARP-2) (NAD(+)) ADP-ribose transferase-2) (Poly(ADP-ribose) synthetase-2) (pADPRT-2) (hPARP-2)	367	e-101
				Q8UGN5	poly(ADP-ribose) polymerase II	366	e-100
				CAB65088.1			
				NP_008758.1	leucine zipper-like transcriptional regulator, 1; Leucine zipper-like regulator-1	996	0
				I54388	LZTR-1	996	0
				BAA07508.1	LZTR-1	996	0
				AAH26214.1	leucine zipper-like transcriptional regulator 1	995	0
				NP_067075.1	RAB18, member RAS oncogene family; RAB18 small GTPase	414	e-116
				Q9NP72	RB18_HUMAN Ras-related protein Rab-18	414	e-116
				AAF61433.1	AF137372_1 ras-related protein RAB18	414	e-116
				CAB86486.1	ras-related small GTPase RAB18	414	e-116
				CAB66668.1	hypothetical protein	414	e-116
				AA049435.1	AF136974_1 ras-related protein 18	414	e-116

			AAH15014.1	AAH15014 RAB18, member RAS oncogene family	414 e-116
			AAM21098.1	AF498950_1 small GTP binding protein RAB18	414 e-116
			AAH29350.1	RAB18, member RAS oncogene family	414 e-116
NM_008732 NP_032758.1	Mm.1304	F(C-D)+ 2.65	P49281	NRM2_HUMAN Natural resistance-associated macrophage protein 2 (NRAMP 2)(Divalent metal transporter 1) (DMT1)	
			AAC21459.1	natural resistance-associated macrophage protein 2 non-IRE form	894
			AAC21461.1	natural resistance-associated macrophage protein 2	894
			BAB93467.1	natural resistance-associated macrophage protein 2 non-IRE form	894
			CAD38517.1	divalent metal transporter	869
			NP_000608.1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2; natural resistance-associated macrophage protein 2	855
			BAA24933.1	NRAMP2	855
			AAC21460.1	natural resistance-associated macrophage protein 2	855
			AAC18078.1	NRAMP2 iron transporter	855
			AAH02592.1	AAH02592 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	855
			BAA34374.1	natural resistance-associated macrophage protein 2	823
			I57022	integral membrane protein	790
			AA479219.1	integral membrane protein	790
			P49279	NRM1_HUMAN Natural resistance-associated macrophage protein 1 (NRAMP 1)	
			I55679	integral membrane protein	605 e-173
			AAA57521.1	integral membrane protein	605 e-173
			BAA08908.1	Nramp	605 e-173

			AAG15405.1	natural resistance-associated macrophage protein 1	605 e-173	
			BAA08907.1	Nramp	605 e-172	
			JC4095	natural resistance-associated macrophage protein NRAMP 1	595 e-169	
				solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; natural resistance-associated macrophage protein 1 (might include Leishmaniasis); solute carrier family 11 (sodium/phosphate symporters), member 1		
			NP_000569.1		593 e-169	
			CAA57541.1	NRAMP	593 e-169	
			BAA07370.1	Nramp	556 e-158	
				erythrocyte protein band 4.1-like 4	1032	0
			NP_071423.1	NBL4_HUMAN Band 4.1-like protein 4	1032	0
			Q9HCS5		1032	0
			BAB17229.1	hNBL4	1032	0
			BAC04690.1	unnamed protein product	382 e-105	
			AAH31042.1	Similar to erythrocyte protein band 4.1-like 4	377 e-104	
			AAH32822.1	Unknown (protein for MGC:26029)	273	6e-73
			Q9HCM4	YF48_HUMAN Hypothetical protein KIAA1548	273	6e-73
			NP_085960.1	KIAA1548 protein	273	6e-73
			BAB14360.1	unnamed protein product	273	6e-73
			NP_061987.2	erythrocyte membrane protein band 4.1 like 4B; EHM2 gene; FERM-containing protein	267	6e-71
			AAQ43366.1	AF153416_1 FERM-containing protein	267	6e-71
			AAQ43366.1	AF153418_1 FERM-containing protein	267	6e-71
			BAA96079.2	similar to mouse Ehm2	267	6e-71
				protein tyrosine phosphatase; non-receptor type 4; megakaryocyte phosphatase; PTPase-MEG1; protein tyrosine phosphatase MEG1; megakaryocyte protein-tyrosine phosphatase		
			NP_002821.1		265	3e-70

			P29074	PTN4_HUMAN Protein tyrosine phosphatase, non-receptor type 4 (Protein-tyrosine phosphatase MEG1) (PTPase-MEG1) (MEG)	285	3e-70
			A41105	protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, non-receptor type 4	285	3e-70
			AAA36530.1	protein-tyrosine phosphatase	285	3e-70
			AAH10674.1	AAH10674 protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	285	3e-70
NM_010050				type 2 iodothyronine deiodinase	480	e-135
NP_034180.1	Mm.21389	F:(C-D)+ 2.64	AAC95470.1	IOD2_HUMAN Type II iodothyronine deiodinase (Type-II 5'deiodinase) (DIOII) (Type 2 DII) (SDII)	477	e-134
			Q92813	deiodinase, iodothyronine, type II; thyroxine deiodinase, type II	469	e-131
			NP_054644.1	deiodinase, iodothyronine, type II; thyroxine deiodinase, type II	469	e-131
			NP_000784.2	deiodinase, iodothyronine, type II; thyroxine deiodinase, type II	469	e-131
			AAC50663.1	type II iodothyronine deiodinase	469	e-131
			AAD45494.1	AC007372_1 type 2 iodothyronine deiodinase	469	e-131
			BAB16838.1	type II iodothyronine deiodinase	449	e-125
NM_009010				UV excision repair protein RAD23 homolog A; RAD23, yeast homolog, A; RAD23 homolog A	562	e-160
NP_033036.1	Mm.41084	F:(C-D)+ 2.64	NP_005044.1	R23A_HUMAN UV excision repair protein RAD23 homolog A (HHR23A)	562	e-160
			P54725	RAD23 protein homolog2	562	e-160
			S44443	HHR23A protein	562	e-160
			BAA04767.1	human RAD23A homolog	562	e-160
			AAB51177.1	AAH14026 Similar to RAD23 (S. cerevisiae) homolog A	562	e-160
			AAH14026.1	RAD23 homolog A (S. cerevisiae)	562	e-160
			AAN39383.1		562	e-160

					UV excision repair protein RAD23 homolog B; XP-C repair complementing protein; XP-C repair complementing complex 58 kDa; RAD23, yeast homolog of, B	NP_002865.1	352	5e-97
					R23B_HUMAN UV excision repair protein RAD23 homolog B (HHR23B) (XP-C repair complementing complex 58 kDa protein) (P58)	P54727	352	5e-97
					RAD23 repair homolog	S44346	352	5e-97
					XP-C repair complementing protein (p58/HHR23B)	BAA04652.1	352	5e-97
					bA131A5.1 (similar to S.cerevisiae RAD23)	CAD13275.1	352	5e-97
					RAD23 homolog B (S. cerevisiae)	AAN47194.1	352	5e-97
					AAH20973.1 RAD23 homolog B (S. cerevisiae)	AAH20973.1	352	5e-97
					similar to UV excision repair protein RAD23 homolog B (HHR23B) (XP-C repair complementing complex 58 kDa protein) (P58)	XP_067249.4	351	1e-96
							254	1e-67
D63902			F:(C-D)+ 2.63		zinc finger protein 147; Zinc finger protein-147; estrogen-responsive finger protein; tripartite motif protein TRIM25; tripartite motif-containing 25	NP_005073.1	941	0
BAA00941.1		Mm.4973	F:(C-HI) +3		Z147_HUMAN Zinc finger protein 147 (Tripartite motif protein 25) (Estrogen responsive finger protein) (Efp)	Q14258	941	0
					estrogen-responsive finger protein, efp (RING finger, coiled-coil domains)	A49656	941	0
					estrogen responsive finger protein	BAA04747.1	941	0
					zinc finger protein 147 (estrogen-responsive finger protein)	AAH16924.1	941	0
					Similar to zinc finger protein 147 (estrogen-responsive finger protein)	AAH42541.1	941	0
							941	0
AK006835			F:(C-D)+ 2.63		HMG box containing protein 1	AAC08317.1	551	0
NP_594876.1		Mm.87639			AF182038_1 HMG box-containing protein 1a	AAC56225.1	551	0
					HMG-box containing protein 1	NP_036389.2	551	0
					AAH17069.1 Unknown	AAH17069.1	551	0

				AAH2329.1	Unknown (protein for MGC:22757)	547	0
				AA871862.1	HMG box containing protein 1	540	0
				BAB85059.1	unnamed protein product	551	0
NM_011340					AAH00522 Similar to serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antipainin, pigment epithelium derived factor), member 1	659	0
NP_035470.1			F:(C-D)+ 2.62 Mm.2044	AAH00522.1	PEDF HUMAN Pigment epithelium-derived factor precursor (PEDF) (EPC-1)	659	0
				P38955	AF400442_1 pigment epithelium-derived factor	659	0
				AAK32491.1	pigment epithelial-differentiating factor precursor	657	0
				A47281	pigment epithelial-differentiating factor	657	0
				AAA60068.1	pigment epithelial-differentiating factor	656	0
				11MV	A Chain A, 2.85 A Crystal Structure Of Pedf	655	0
				AAH13984.1	AAH13984 Unknown (protein for MGC:20155)	603	e-172
				A46046	serine proteinase inhibitor homolog EPC-1	580	e-165
				NP_002606.1	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antipainin, pigment epithelium derived factor), member 1; pigment epithelium-derived factor	545	e-155
				AAA84914.1	pigment epithelium-derived factor	501	e-142
				AA836885.1	EPC-1	632	e-180
				NP_005054.2	stearoyl-CoA desaturase (delta-9-desaturase)	632	e-180
				AAD29870.	AF097514_1 stearoyl-CoA desaturase	632	e-180
				BAA93510.1	stearoyl-CoA desaturase	633	e-180
				O00767	ACOD_HUMAN Acyl-CoA desaturase (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase)	626	e-178
				AAH05807.1	AAH05807 Unknown (protein for MGC:10284)	624	e-178
				CAAT3998.1	stearoyl CoA desaturase	590	e-168
				AAF11040.1	AF116721_18 PRO0998	413	e-114
				IS4779	stearoyl-CoA desaturase	413	e-114
				AA830631.1	stearoyl-CoA desaturase, delta-9-desaturase	413	e-114

				XP_208174.1	similar to stearyl-CoA desaturase	288	5e-71
				NP_079182.1	hypothetical protein FLJ21032	214	9e-55
				BAB14961.1	unnamed protein product	214	9e-55
				CAD38567.1	hypothetical protein	206	2e-52
AI156588							
XP_125732	Mm.100614	F:(C-D)+ 2.61		AAH11761.1	AAH11761 Unknown (protein for MGC:19749)	274	3e-74
				NP_006835.2	ilvB (bacterial acetoacetylase synthase)-like isoform 1; acetoacetylase synthase homolog	274	3e-74
				AAB94632.1	acetoacetylase synthase	274	3e-74
				AAH11722.1	AAH11722 Unknown	274	3e-74
				AAC50934.1	acetoacetylase synthase homolog	271	3e-74
				AAC18916.1	Acetoacetylase synthase	201	5e-52
NM_008160							
NP_032186.1	Mm.1090	F:(C-D)+ 2.6		NP_000572.1	glutathione peroxidase 1	352	5e-97
				CAA68491.1	glutathione peroxidase	352	5e-97
				CAA31983.1	opal codon coding for selenocysteine	352	5e-97
				P07203	GSHC_HUMAN Glutathione peroxidase (GSHPx-1) (Cellular glutathione peroxidase)	352	5e-97
				CAB37833.1	glutathione peroxidase	352	5e-97
				CAA31892.1	glutathione peroxidase	349	3e-96
				OPHUE	glutathione peroxidase (EC 1.11.1.9) 1	347	1e-95
				AAAT5389.2	glutathione peroxidase	344	1e-94
				AAA67540.2	glutathione peroxidase	340	2e-93
				XP_208432.1	similar to glutathione peroxidase 1	336	2e-92
				P18283	SHG_HUMAN Glutathione peroxidase-gastrointestinal (GSHPx-GI) (Glutathione peroxidase-related protein 2) (Gastrointestinal glutathione peroxidase) (GPRP)	248	8e-66
				A45207	glutathione peroxidase (EC 1.11.1.9) 2	248	8e-66
				NP_002074.1	gastrointestinal glutathione peroxidase 2	248	8e-66

				CAA48394.1	glutathione peroxidase-GI	248	8e-66
				AAF74026.1	AF199441_1 gastrointestinal glutathione peroxidase	240	2e-63
			F:(C-D)+ 2.58				
AK005070			F:(C-HI) +3.04		solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1; solute carrier family 20 (mitochondrial citrate transporter), member 3		
XP_110162	Mm.22679			NP_005975.1	TXTP_HUMAN Tricarboxylate transport protein, mitochondrial precursor (Citrate transport protein) (CTP) (Tricarboxylate carrier protein)	492	e-139
				P53007	Similar to solute carrier family 25 (mitochondrial carrier; citrate transporter) member 1	492	e-139
				AAH04980.1	Unknown (protein for MGC:2151)	492	e-139
				AAH08061.1	L75823_1 citrate transport protein	492	e-139
				AAL40090.1	L76134_1 citrate transport protein	492	e-139
				AAL40091.1	mitochondrial citrate transport protein	498	e-138
				CAA65633.1	citrate transporter protein	489	e-138
				G01789	citrate transporter protein	489	e-138
				AAB08515.1			
NM_022417			F:(C-D)+ 2.58		integral membrane protein 3; E25 protein	413	e-115
NP_071862.1	Mm.29870		F:(C-HI) +2.6	NP_112188.1	ITMC_HUMAN Integral membrane protein 2C (Transmembrane protein 2C)	413	e-115
				Q9NQX7	BRB3 (NP0018)	413	e-115
				AAF89492.1	AF272043_1 BRB3	413	e-115
				AAG44792.1	AF271781_1 NP0018	413	e-115
				CAB66538.1	hypothetical protein.	413	e-115
				AAL15434.1	BRB3	413	e-115
				BAC11570.1	unnamed protein product	413	e-115
				AAH02424.1	AAH02424: Similar to integral membrane protein 3	410	e-114

		BAB46927.1	cerebral protein-14	410	e-114
		CAD28460.1	hypothetical protein	410	e-114
		BAC03562.1	unnamed protein product	397	e-110
		AAH25742.1	Similar to integral membrane protein 3	315	1e-85
NM_011829	F:(C-D)+	P20839	IMD1_HUMAN Inosine-5'-monophosphate dehydrogenase 1 (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1)	984	0
NP_036959.1	Mm.45234	AAH33622.1	IMP (inosine monophosphate) dehydrogenase 1	984	0
		A35566	IMP dehydrogenase (EC 1.1.1.205) I	979	0
		NP_000874.1	IMP (inosine monophosphate) dehydrogenase 1; sWSS2608	973	0
		AAA36114	IMP dehydrogenase type 1 (EC 1.1.1.205)	973	0
		BAB70780.1	unnamed protein product	917	0
		XP_093044.1	similar to IMP dehydrogenase (EC 1.1.1.205) I	876	0
		P12268	IMD2_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2) (IMPDH-II) (IMPD 2)	860	0
		A31997	IMP dehydrogenase (EC 1.1.1.205) II	860	0
		1B30	A Chain A, Ternary Complex Of Human Type-II Inosine Monophosphate Dehydrogenase With 6-Cl-IMP And Selenazole Adenine Dinucleotide	880	0
		1B30	B Chain B, Ternary Complex Of Human Type-II Inosine Monophosphate Dehydrogenase With 6-Cl-IMP And Selenazole Adenine Dinucleotide	860	0
		AAA67054.1	inosine monophosphate dehydrogenase type II	860	0
		AAB70699.1	inosine monophosphate dehydrogenase type II	860	0
		AAH06124.1	AAH06124 IMP (inosine monophosphate) dehydrogenase 2	860	0
		AAH12840.1	AAH12840 IMP (inosine monophosphate) dehydrogenase 2	860	0
		AAH15567.1	AAH15567 IMP (inosine monophosphate) dehydrogenase 2	860	0

				NP_000876.1	IMP (inosine monophosphate) dehydrogenase 2; IMP (inosine 5'-phosphate) dehydrogenase-2	856	0
				NP_000875.1	inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	856	0
				XP_067686.1	similar to inosine-5'-monophosphate dehydrogenase 1 (IMP dehydrogenase 1) (IMPDH-1) (IMPD 1)	517 e-146	
				XP_167188.1	similar to inosine-5'-monophosphate dehydrogenase 1 (IMP dehydrogenase 1) (IMPDH-1) (IMPD 1)	511 e-145	
				XP_066634.2	similar to inosine-5'-monophosphate dehydrogenase 1 (IMP dehydrogenase 1) (IMPDH-1) (IMPD 1)	481 e-135	
NM_018868 NP_061356.1	Mm.10303	F:(C-D)+ 2.57		NP_057018.1	nucleolar protein NOP5/NOP58	812	0
				Q9Y2X3	NOP5_HUMAN Nucleolar protein NOP5 (Nucleolar protein 5) (NOP58) (HSPC120)	812	0
				AAD27610.1	AF123534_1 nucleolar protein NOP5/NOP58	812	0
				AAF91394.1	AF263608_1 nucleolar protein	812	0
				AAH32592.1	nucleolar protein NOP5/NOP58	812	0
				T17299	hypothetical protein DKFZp564H2171.1 - human	766	0
				CAB55989.1	hypothetical protein	766	0
				AAF29084.1	AF161469_1 HSPC120	621 e-177	
				O00567	NO56_HUMAN Nucleolar protein Nop56 (Nucleolar protein 5A)	304	2e-82
				NP_006383.1	nucleolar protein 5A (56kDa with KKE/D repeat); nucleolar protein (KKE/D repeat); nucleolar protein 5A (56kDa with KKE/D repeat)	304	2e-82
				CAAT72789.1	hNop56	304	2e-82
				CAC01444.2	dJ686C3.2 (nucleolar protein NOP56)	302	2e-81
NM_011571 NP_035701.1	Mm.10154	F:(C-D)+ 2.56		AAH38448.1	Similar to testis-specific kinase 1	744	0
				NP_006276.1	testis-specific protein kinase 1	742	0

			Q15569	TES1_HUMAN Testis-specific protein kinase 1 (Testicular protein kinase 1)	742	0
			BAA09459.1	TESK1	742	0
			AAM05015.1	testis-specific kinase-1	313	4e-85
			Q06S83	TES2_HUMAN Testis-specific protein kinase 2	291	2e-78
			BAB82909.1	testicular protein kinase 2	291	2e-78
			AAM177909.1	testis specific kinase-1	281	2e-75
			NP_009101.1	testis-specific protein kinase 2	247	4e-85
			CAB41970.1	protein kinase	247	4e-85
NM_010587						
NP_034717.1	Mm.40546	F:(C-D)+ 2.56	AAD29952.1	AF114487_1 intersectin long isoform	2355	0
		*	Q15811	ITN1_HUMAN Intersectin 1 (SH3 domain-containing protein 1A)(SH3P17)	2352	0
			NP_003015.1	intersectin 1 (SH3 domain protein); SH3 domain protein-1A; Intersectin (SH3 domain protein 1A); human Intersectin-SH3 domain-containing protein SH3P17	2350	0
			NP_062541.2	intersectin 2 isoform 3; SH3 domain protein 1B; SH3P18-like WASP associated protein	1437	0
			BAA88570.1	KIAA1256 protein	1436	0
			AAF63600.1	AF248540_1 intersectin 2	1436	0
			NP_006268.1	intersectin 2 isoform 1; SH3 domain protein 1B; SH3P18-like WASP associated protein	1423	0
			Q9NZM3	ITN2_HUMAN Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein)	1423	0
			AAF59903.1	AF182198_1 Intersectin 2 long isoform	1420	0
			AAD29953.1	AF114488_1 intersectin short isoform	1349	0
			AAC78610.1	intersectin short form	1348	0
				peroxisomal lon protease	1491	0
NM_025827			CAD68987.1	unnamed protein product	1489	0
NP_080103.1	Mm.30092	F:(C-D)+ 2.54	BAC11201.1			

			CAD38889.1	hypothetical protein	1229	0
			NP_113678.1	hypothetical protein MGC4840	1039	0
			BAB5278.1	unnamed protein product	1039	0
			CAA52291.1	Lon protease-like protein	418	e-116
			S42366	endopeptidase La homolog (EC 3.4.21.-) precursor, mitochondrial (version 2)	418	e-116
			CAA53625.1	Lon protease-like protein	418	e-116
			2007252A	ATP-dependent lon protease	418	e-116
			NP_004784.	protease, serine, 15; Lon protease-like protein; hLON ATP-dependent protease; LON protease	418	e-116
			P36776	LONM_HUMAN Lon protease homolog, mitochondrial precursor (Lon protease-like protein) (LONP) (LONHs)	417	e-116
			AAD24414.1	AF059309.1 LON protease	417	e-116
			AAH00235.1	AAH00235 protease, serine, 15	417	e-116
			BAC04829.1	unnamed protein product	417	e-116
			S57342	endopeptidase La homolog (EC 3.4.21.-) precursor, mitochondrial (version 1)	413	e-115
			AAA61616.1	hLON ATP-dependent protease	413	e-115
			AAH04934.1	AAH04934 Unknown (protein for IMAGE:3606377)	408	e-113
NM_016896		F:(C-D)+	NP_002072.1	glypican 1 precursor	934	0
NP_057905.1	Mm.24193	2.54	P35052	GPC1_HUMAN Glypican-1 precursor	934	0
			A36347	glypican 1 precursor	934	0
			CAA38139.1	glypican	934	0
			1704260A	heparan sulfate proteoglycan	934	0
			NP_005699.1	glypican 6 precursor	934	0
			Q9Y625	GPC6_HUMAN Glypican-6 precursor	490	e-138
					490	e-138

		AAD31392.1	AF111178_1	glypican-6	490	e-138
		AAD55749.1	AF105267_1	glypican-6	490	e-138
		NP_001432.2		glypican 4	445	e-124
		AAH17166.1		similar to glypican 4	445	e-124
		OT5487		GPC4_HUMAN Glypican-4 precursor (K-glypican)	444	e-124
		AAC31899.1		glypican 4	444	e-124
		AAC68991.1		glypican-4	443	e-124
		AAL11018.1		glypican-4	443	e-124
		NP_689955.1		glypican 2; cerebroglycan	362	3e-99
		AAH27972.1		Glypican 2	362	3e-99
		CAD39080.1		hypothetical protein	362	3e-99
		BAC04745.1		unnamed protein product	362	3e-99
NM_010028				DDX3_HUMAN DEAD-box protein 3 (Helicase-like protein 2) (HLP2)		
NP_034158.1	Mm.88188	F:(C-D)+ 2.54	O00571	(DEAD-box, X isoform)	1038	0
			AAH95637.1	helicase like protein 2	1038	0
			AAC34298.1	DEAD box RNA helicase DDX3	1038	0
			AAH11819.1	AAH11819 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	1038	0
				DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3; DEAD/H box-3;		
			NP_001347.2	helicase like protein 2; CAP-Rf	1036	0
			NP_076829.1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3; DEAD/H box-3;	1036	0
				helicase like		
				protein 2;		
			CAP-Rf		1036	0
			AAC51829.1	dead box, X isoform	1036	0
			AAC51830.1	dead box, X isoform	1036	0

			NP_004651.2	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome; DEAD/H box-3, Y-linked	988	0
			AAH34942.1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome	988	0
			O15523	DDXY_HUMAN DEAD-box protein 3, Y-chromosome	986	0
			AAC51831.1	dead box, Y isoform	986	0
			AAC51832.1	dead box, Y isoform	986	0
			NP_061912.1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 4; VASA protein	441 e-123	
			NP_077726.1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 4; VASA protein	441 e-123	
			Q9NQI0	DDX4_HUMAN DEAD-box protein 4 (VASA homolog)	441 e-123	
			AAF72705.1	VASA protein	441 e-123	
			T46407	probable RNA helicase protein DKFZp434B122.1	441 e-123	
			CAB70750.1	hypothetical protein	441 e-123	
			AAF86585.1	DEAD box RNA helicase	439 e-123	
			AAH47455.1	DDX4 protein	439 e-122	
				similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3; D-E-A-D (aspartate-glutamate-alanine-aspartate) box polypeptide 3; DEAD helicase [Mus musculus]	383 e-109	
			XP_066968.2	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 isoform 1; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD); probable RNA-dependent helicase p72	322	3e-87
			NP_006377.1	DDI7_HUMAN Probable RNA-dependent helicase p72 (DEAD-box protein p72) (DEAD-box protein 17)	322	3e-87
			Q92841	ATP-dependent RNA helicase	322	3e-87
			S72367	DEAD-box protein p72	322	3e-87
			AAC50787.1	DEAD-box protein p72	322	3e-87
			AAH00595.1	AAH00595 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD)	322	3e-87

NM_021446 NP_067421.1	Mm.143795	F:(C-D) ⁺ 2.54	AAF28966.1	AF161406_1 HSPC288	286	5e-77
			NP_009107.1	chromosome 14 open reading frame 1	278	1e-74
			Q9UKR5	CN01_HUMAN Protein C14orf1 (HSPC288) (Protein AD-011) (x0006)	278	1e-74
			AAD54079.1	AF134159_1 potential membrane protein C14orf1	278	1e-74
			CAB66593.1	hypothetical protein	278	1e-74
			AAG49432.1	AF136971_1 proteinox0006	278	1e-74
			AAH02444.1	AAH02444 chromosome 14 open reading frame 1	278	1e-74
			CAD62345.1	unnamed protein product	275	7e-74
			AAD51373.1	AC007182_2 unknown	244	2e-64
AK007857 XP_125913.2	Mm.158320	F:(C-D) ⁺ 2.54	NP_883895.1	orphan short-chain dehydrogenase / reductase; retinol dehydrogenase similar protein	358	1e-98
			AAK95856.1	retinol dehydrogenase similar protein	358	1e-98
			AAC39922.1	sterol/retinol dehydrogenase	222	6e-58
			NP_003699.2	mitochondrial NAD+-dependent retinol dehydrogenase 4	217	2e-56
			AAC72923.1	retinol dehydrogenase	217	2e-55
				3-hydroxysteroid epimerase; oxidative 3-alpha-hydroxysteroid-dehydrogenase; 3(alpha->beta)-hydroxysteroid epimerase; retinol dehydrogenase; oxidoreductase; NAD+-dependent 3 alpha-hydroxysteroid dehydrogenase	204	2e-52
			NP_003716.2	alpha-hydroxysteroid dehydrogenase	204	2e-52
			AAB67236.1	oxidoreductase	204	2e-52
			AAF81017.1	AF223225_1 3-hydroxysteroid epimerase	204	2e-52
			AAH20710.1	AAH20710 oxidative 3 alpha hydroxysteroid dehydrogenase; retinol dehydrogenase; 3-hydroxysteroid epimerase	204	2e-52
			AAH28298.1	Similar to retinol dehydrogenase 5 (11-cis and 9-cis)	200	3e-51

			Q92781	RDH1_HUMAN 11-cis retinol dehydrogenase (11-cis RDH)	200	3e-51
			AAC50725.1	11-cis retinol dehydrogenase	200	3e-51
			AAC09250.1	retinol dehydrogenase	200	3e-51
		F:(C-D)+ 2.52 F:(C-H) +3.43				
NM_011817 NP_035947.1	Mm.8653		BAA84543.1	gadd45-related protein	313	2e-85
			NP_006896.1	growth arrest and DNA-damage-inducible, gamma; GADD45-gamma; gadd-related protein, 17 kD	307	1e-83
			O95257	G45G_HUMAN Growth arrest and DNA-damage-inducible protein GADD45 gamma	307	1e-83
			AAC83329.1	growth arrest and DNA-damage-inducible protein GADD45gamma	307	1e-83
			AAD28544.1	AF079806_1 cytokine responsive protein	307	1e-83
			AAF73468.1	AF265659_1 GADD45 gamma	307	1e-83
			AAH00485.1	growth arrest and DNA-damage-inducible, gamma	307	1e-83
			AAH19325.1	growth arrest and DNA-damage-inducible, gamma	307	1e-83
			AAM00007.1	AF494037_1 growth arrest and DNA-damage-inducible, gamma	307	1e-83
			AAK00414.1	AF087883_1 growth arrest and DNA damage inducible protein gamma	303	3e-82
				phosphoribosylaminoimidazole carboxylase; phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase; AIR carboxylase; SAICAR synthetase	839	0
NM_025939 NP_080215.1	Mm.182931	F:(C-D)+ 2.52 F:(C-H) +2.69	NP_006443.1	PUR6_HUMAN Multifunctional protein ADE2 [includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (AIR carboxylase) (AIRC)]	839	0
			P22234		839	0
			S14147	multifunctional purine biosynthesis protein	839	0

			CAA37801.1	5' half of the product is homologues to <i>Bacillus subtilis</i> SAICAR synthetase, 3' half corresponds to the catalytic subunit of AIR carboxylase synthetase	839	0
			AAH10273.1	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	839	0
			AAH19255.1	AAH19255 multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase	839	0
AA409743 XP_129542.1	F:(C-D)+ 2.52	Mm.22632	AAG01993.1	similar to Homo sapiens mRNA for KIAA0120 gene with GenBank Accession Number D21261.1	221	1e-58
			NP_003555.1	transgelin 2; SMZ2-alpha homolog	221	1e-58
			P37802	TAG2_HUMAN Transgelin 2 (SMZ2-alpha homolog)	221	1e-58
			BAA04802.1	KIAA0120	221	1e-58
			AAH09357.1	AAH09357 transgelin 2	221	1e-58
			AAH02616.1	AAH02616 transgelin 2	219	6e-58
NM_025879 NP_080155.2	F:(C-D)+ 2.5	Mm.12755	NP_079217.1	hypothetical protein FLJ13811	616	e-176
			BAB14633.1	unnamed protein product	616	e-176
			AAH12006.1	AAH12006 Similar to RIKEN cDNA 2410002O22 gene	396	e-130
			CAD28498.1	hypothetical protein	330	5e-90
NM_033354 NP_203505.1	F:(C-D)+ 2.5	Mm.87114	NP_149118.1	regucalcin gene promoter region related protein; RGPR-p117	1282	0
			BAB61035.1	RGPR-p117	1282	0
			BAB67821.1	KIAA1928 protein	940	0
			BAC03392.1	FLJ00305 protein	881	0
			AAH09106.1	AAH09106 Unknown (protein for MGC:17455)	855	0
			BAC05357.1	unnamed protein product	478	e-134
			XP_088459.6	similar to KIAA0310 protein	429	e-119

				AAH28183.1	nkown (protein for IMAGE:4508322)	429 e-119
				O15027	Y310_HUMAN Hypothetical protein KIAA0310	429 e-119
				BAA20769.3	KIAA0310 protein	429 e-119
				AAH08332.1	AAH08332 Unknown (protein for IMAGE:3505732)	295 3e-79
NM_008471		F-(C-D)+		P08727	K1CS_HUMAN Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	539 e-153
NP_032497.1	Mm.1012	1.85		CAA68566.1	Keratin 19 (AA 1 - 399)	539 e-153
				AAF27048.1	keratin 19	539 e-153
				NP_002287.2	keratin 19; keratin, type I cytoskeletal 19; keratin, type I, 40-kD cytokeratin 19; 40-kDa keratin intermediate filament precursor gene	539 e-153
				AAH10409.1	AAH10409 Unknown (protein for MGC:15368)	539 e-153
				KRHU9	keratin 19, type I, cytoskeleton	539 e-153
				AAA36044.1	40-kDa keratin protein	539 e-153
				AAH02539.1	AAH02539 keratin 19	539 e-153
				AAH07628.1	AAH07628 keratin 19	539 e-153
				NP_000413.1	keratin 17	453 e-127
				Q04695	K1CO_HUMAN Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1)	453 e-127
				S30433	keratin 17, type I, cytoskeletal	453 e-127
				CAA79626.1	cytokeratin 17	453 e-127
				CAA44451.1	keratin related product	453 e-127
				AAH00159.2	AAH00159 keratin 17	453 e-127
				AAH11901.1	AAH11901 Similar to keratin 17	453 e-127
				BAC04534.1	unnamed protein product	453 e-127
				KRHUE	keratin 14, type I, cytoskeletal	443 e-124

	AAB59562.1	keratin		443 e-124
	AAH02690.1	AAH02690 keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)		443 e-124
	AAH19097.1	AAH19097 keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)		443 e-124
	NP_000517.2	keratin 14; cyokeratin 14		443 e-124
	P02533	K1CN_HUMAN Keratin, type I cytoskeletal 14 (Cyokeratin 14) (K14) (CK 14)		
	AAH42437.1	similar to keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)		443 e-124
	NP_002266.2	keratin 15; keratin-15, basic; keratin-15, beta; type I cytoskeletal 15; cyokeratin 15		442 e-124
	AAH02641.1	AAH02641 keratin 15		442 e-124
	PI9012	K1CO_HUMAN Keratin, type I cytoskeletal 15 (Cyokeratin 15) (K15) (CK 15)		442 e-124
	KRHU5	keratin 15, type I, cytoskeletal		442 e-124
	CAA30535.1	cytokeratin 15 (AA 1 - 456)		442 e-124
	AAF27047.1	keratin 15		442 e-124
		argininosuccinate synthetase	793	0
	NP_446464.1	ASSY_HUMAN Argininosuccinate synthase (Citrulline--aspartate ligase)	793	0
	P00966	AAH09243 argininosuccinate synthetase	793	0
	AAH09243.1	AAH09243 argininosuccinate synthetase	793	0
	AAH21676.1	AAH21676 Unknown (protein for MGC:22864)	793	0
	AAK67487.1	argininosuccinate synthetase	793	0
	NP_000041.1	argininosuccinate synthetase	781	0
	AJHURS	argininosuccinate synthase (BC 6.3.4.5)	781	0
	CAA25771.1	argininosuccinate synthetase (aa 1-412)	781	0

		AAA51783.1	argininosuccinate synthetase	781	0
		XP_210236.1	similar to argininosuccinate synthetase	434	e-121
		XP_095989.1	similar to argininosuccinate synthetase	253	4e-67
		AAB96328.1	argininosuccinate synthase (citrulline-aspartate ligase); 84% Similarity to P09034 (NID:g114291)	231	2e-60
		XP_070116.1	similar to argininosuccinate synthase (citrulline-aspartate ligase); 84% Similarity to P09034 (NID:g114291)	218	2e-56
NM_021099	F(C-D)+ 1:74	AAC50969.1	KIT protein	1531	0
NP_066922.1	Mm.4394	NP_000213.1	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog precursor	1526	0
		P10721	KIT, HUMAN Mast/stem cell growth factor receptor precursor (SCFR) (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen)	1526	0
		TVHUKT	protein-tyrosine kinase (BC 2.7.1.112), receptor type kit precursor human	1526	0
		CAA29548.1	protein p145-ckit (AA.1 - 976)	1526	0
		CAA49159.1	mast/stem cell growth factor receptor	1526	0
		AAC50968.1	KIT protein	1526	0
		CAA27300.1	put. c-fms precursor	647	0
		NP_005202.2	colony stimulating factor 1 receptor precursor; FMS proto-oncogene; CD115 antigen; macrophage colony stimulating factor 1 receptor; similar to mouse Friend murine leukemia virus integration site 2	647	0
		P07333	KFMS HUMAN Macrophage colony stimulating factor I receptor precursor (CSF-1-R) (Fms proto-oncogene) (c-fms) (CD115 antigen)	647	0
		TVHUMD	macrophage colony-stimulating factor 1 receptor precursor	647	0
		AAB51696.1	CSF-1 receptor	647	0

			1204266A	gene c-fms		647	0
			AAH47521.1	Colony stimulating factor 1 receptor, precursor		645	0
			NP_006197.1	platelet-derived growth factor receptor alpha precursor		511	e-144
			P16234	PGDS_HUMAN Alpha platelet-derived growth factor receptor precursor PDGF-R-alpha (CD140a antigen)		511	e-144
			PFHUGA	platelet-derived growth factor receptor alpha precursor		511	e-144
			AAA60048.1	platelet-derived growth factor A receptor		511	e-144
			AAA96715.1	platelet-derived growth factor receptor A chain		511	e-144
			BAA08742.1	alpha-platelet-derived growth factor receptor		511	e-144
			AAA36427.1	platelet-derived growth factor receptor		484	e-136
			NP_002600.1	platelet-derived growth factor receptor beta precursor; beta platelet-derived growth factor receptor		484	e-136
			P09619	GDR_HUMAN Beta platelet-derived growth factor receptor precursor (PDGF-R-beta) CD140b antigen)		484	e-136
			PFHUGB	platelet-derived growth factor receptor beta precursor		484	e-136
			AAA60049.1	platelet-derived growth factor receptor		484	e-136
			AAH32224.1	platelet-derived growth factor receptor, beta polypeptide		483	e-135
			CAA81393.1	FLT3 receptor tyrosine kinase		442	e-123
AK007692		F:(C-D)+	NP_004297.1	mxn1 A13; annexin XIII; annexin, intestine-specific		223	2e-58
BAB25193.1	Mm.46285	1.62	P27216	NXD_HUMAN Annexin A13 (Annexin XIII) (Annexin, intestine-specific) (ISA)		223	2e-58
			UHUJIS	mxn1 XIII, intestinal [validated]		223	2e-58
			CAA75758.1	intestine-specific annexin		223	2e-58
			CAC34622.1	annexin A13 isoform b		223	2e-58

AK012581		F ₁ (G-D) ⁺	AAK67834.1	hypothetical protein SB143	240	2e-63
BAC25371.1	Mm.21887	1.60	NP_085053.1	hypothetical protein MGC10886	240	2e-63
			AAH04400.1	AAH04400 Unknown (protein for MGC10886)	240	2e-63
			BAC03855.1	unnamed protein product	240	2e-63

Subtable 1B: Unfavorable Mouse Genes/Proteins and Corresponding Human Proteins

NM_009043	U:(C-D)30.27				LITA, HUMAN Lithostathine 1 alpha precursor (Pancreatic stone protein) (PSP) (Pancreatic thread protein) (PTP) (Islet of Langerhans regenerating protein) (REG) (Regenerating protein 1 alpha) (Islet cells regeneration factor) (ICRF)	241	8e-64
NP_033069.1	U:(C-HD)3	P05451			regenerating islet lectin 1: alpha precursor [validated]	241	8e-64
		RGHU1A			islet regenerating protein	241	8e-64
		AAA36558.1			AF172331, 1 lithostathine	241	8e-64
		AAAD51330.1			Regenerating islet-derived 1 alpha, precursor	241	8e-64
		AAH05350.1			reg protein	241	8e-64
		I617122A			regenerating protein (reg)	238	4e-63
		AAA36559.1			pancreatic stone protein precursor	237	9e-63
		A45751			pancreatic stone protein	237	9e-63
		AAA60546.1			regenerating islet-derived 1 beta precursor, lithostathine 1 beta; regenerating protein 1 beta	235	4e-62
		NP_006498.1			regenerating islet-derived 1 beta precursor (Regenerating protein 1 beta)	235	4e-62
		P48304			LITB, HUMAN Lithostathine 1 beta precursor, lithostathine 1 beta; regenerating protein 1 beta	235	4e-62
		RGHU1B			regenerating islet lectin 1-beta precursor	235	4e-62
		BAA04091.1			regenerating protein 1 beta	235	4e-62
		BAA04124.1			regenerating protein 1 beta	235	4e-62
		AAA18204.1			reg gene homologue	235	4e-62
		AAH27895.1			regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein)	235	4e-62
		ILIT			Human Lithostathine	220	2e-57
		IQDD			A Chain A, Crystal Structure Of Human Lithostathine To 1.3 A Resolution	218	8e-57
NM_009863							
NP_033993.1	Mm.20842	U:(C-D)11.89	NP_003494.1		ODC7-like 1; Gsll division cycle 7, S. Cerevisiae, homolog-like 1	879	0

			O00311	CD/C7_HUMAN Cell division cycle 7-related protein kinase (CD/C7-related kinase) (HsCdc7)	879	0
			BAA19962.1	Cdc7-related kinase	879	0
			AA052080.1	Cdc7	879	0
			AA097512.1	HsCdc7	878	0
NM_011036	U:(C-D)9.09			pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	239	2e-63
NP_035166.1	U:(C-H)6.83	Mm_2553	NP_002571.1	pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	239	2e-63
			NP_620354.1	pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	239	2e-63
			NP_620355.1	pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	239	2e-63
			Q06141	PAP1_HUMAN Pancreatitis-associated protein 1 precursor	239	2e-63
			A49616	pancreatitis-associated protein precursor	239	2e-63
			AA024642.1	PAP-H	239	2e-63
			BAA02728.1	PAP homologous protein	239	2e-63
			CAA48605.1	preprotein	239	2e-63
			AAA60020.1	pancreatitis-associated protein	239	2e-63
			AA036776.1	similar to pancreatitis-associated protein	239	2e-63
			I908220A	pancreatitis-associated protein	239	2e-63
			XP_059401.1	similar to pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	239	3e-63
			AAA36415.1	pancreatitis associated protein	235	4e-62
			Q92778	PBCG_HUMAN Pancreatic beta cell growth factor precursor (islet neogenesis associated protein)	209	4e-54
				myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1; Myeloid/lymphoid or mixed-lineage leukemia (trithorax, Drosophila); myeloid/lymphoid or mixed-lineage leukemia (trithorax, Drosophila) homolog; translocated to, 1	785	0
NM_022328	U:(C-D)9		NP_005925.2		785	0
NP_071723.1	U:(C-H)5.73	Mm_148748	BAA03406.1	L7TG19	785	0
			Q03111	ENL_HUMAN ENL protein	780	0

B44265	ENL (translocation)	780	0
AAA58457.1	translocated to HRX in (11;19) leukemia	780	0
NP_004520.1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3; Myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila); myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 3	424	e-118
P42568	AF9 HUMAN AF-9 protein	424	e-118
E9411	AF-9 protein	424	e-118
AAA58361.1	AF-9	424	e-118
AH36089.1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	423	e-118
XP_059401.1	similar to pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	255	6e-68
NP_002571.1	pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	239	3e-63
NP_620354.1	pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	239	3e-63
NP_620355.1	pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	239	3e-63
Q06141	PAP1 HUMAN Pancreatitis-associated protein 1 precursor	239	3e-63
A49616	pancreatitis-associated protein precursor	239	3e-63
AAB24642.1	PAP-H	239	3e-63
BAA02728.1	PAP homologous protein	239	3e-63
CAA48605.1	preprotein	239	3e-63
AAA60020.1	pancreatitis-associated protein	239	3e-63
AAB36776.1	similar to pancreatitis-associated protein	239	3e-63
1908220A	pancreatitis-associated protein	239	3e-63
AAA36415.1	pancreatitis associated protein	237	1e-62
O92778	PBCG HUMAN Pancreatic beta cell growth factor precursor (islet neogenesis associated protein)	2061	3e-53

[illegible]

NP 002830.1	protein tyrosine phosphatase, receptor type, D isoform 1 precursor; protein tyrosine phosphatase, receptor type, delta polypeptide; protein tyrosine phosphatase delta	173	3
P223468	PTPD_HUMAN Protein-tyrosine phosphatase delta precursor (R-PTP-delta)	173	3
A56178	protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor	173	3
AAC41749.1	protein tyrosine phosphatase delta	173	3
NP 560975.1	protein tyrosine phosphatase, receptor type, D isoform 2 precursor; protein tyrosine phosphatase, receptor type, delta polypeptide; protein tyrosine phosphatase delta	173	3
NP 570924.1	protein tyrosine phosphatase, receptor type, sigma isoform 2 precursor; protein tyrosine phosphatase PTP-sigma	138	0
U:(C-D)5.51 U:(EL-D)2.67	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (S cerevisiae CHL1-like helicase); S cerevisiae CHL1-like helicase	112	0
Mm.3935	DD24_HUMAN ATP-dependent RNA helicase DDX24 (DEAD-box protein 24)	112	0
NP 065147.1	AF214731.1 ATP-dependent RNA helicase	112	0
NP 0651507.1	unnamed protein product	112	0
CAB66820.1	hypothetical protein	112	0
AAH08847.1	AAH08847 (Asp-Glu-Ala-Asp/His) box polypeptide 24	112	0
AAH09406.1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24	112	0
U:(C-D)5.5 U:(EL-D)2.54	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial); 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	929	0
NP 005509.1	HMCM_HUMAN Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor (HM-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase)	929	0
NP 005509.1	HMCM_HUMAN Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor (HM-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase)	929	0

			S71623	hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) precursor, mitochondrial	929	0
			CAA58893.1	hydroxymethylglutaryl-CoA synthase [Homo sapiens]	929	0
			AAB72036.1	3-hydroxy-3-methylglutaryl CoA synthase [Homo sapiens]	929	0
			AAH44217.1	similar to 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	929	0
			AAA92674.1	HMG CoA synthase	679	0
				3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble);		
			NP_002121.1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	659	0
			Q01581	HMCS_HUMAN Hydroxymethylglutaryl-CoA synthase, cytoplasmic (HMG-CoA synthase)	659	0
			S45497	(3-hydroxy-3-methylglutaryl coenzyme A synthase)	659	0
			AAA62411.1	hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), cytosolic, adrenal isoform	659	0
			AAH00297.1	3-hydroxy-3-methylglutaryl coenzyme A synthase	659	0
			S27197	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	659	0
			CNA47061.1	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), cytosolic, fibroblast isoform	650	0
			BAC04559.1	Hydroxymethylglutaryl CoA Synthase unnamed protein product	629	e-180
			XP_060842.1	similar to Hydroxymethylglutaryl-CoA synthase, cytoplasmic (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase)	244	4e-64
			AA92673.1	HMG CoA synthase	240	1e-62
				fatty acid binding protein 4, adipocyte; A-FABP	245	4e-65
		U:(C-D)5.33 U:(C-HD)4.36	NP_001433.1	FABA_HUMAN Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding protein) (ALBP) (A-FABP)	245	4e-65
		Mm.582	P15090	fatty acid-binding protein, adipocyte	245	4e-65
			PZHUUF	adipocyte lipid-binding protein	245	4e-65
			AAA51689.1	adipocyte lipid-binding protein 4, adipocyte	245	4e-65
			AAH03672.1	fatty acid binding protein 4, adipocyte	245	4e-65
				pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	223	2e-58
			U:(C-D)5.05 U:(C-HD)3.44			
		Mm.263	NP_002571.1			

AK004839	NP 620354.1	pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	223	2e-58
XP 129259.1	NP 620355.1	pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	223	2e-58
	Q06141	PAP1 HUMAN Pancreatitis-associated protein 1 precursor	223	2e-58
	A49616	pancreatitis-associated protein precursor - human	223	2e-58
	AAE24642.1	PAP-H	223	2e-58
	BAA02728.1	PAP homologous protein	223	2e-58
	CAA48605.1	preprotein	223	2e-58
	AAA60020.1	pancreatitis-associated protein	223	2e-58
	AAH36776.1	similar to pancreatitis-associated protein	223	2e-58
	I908220A	pancreatitis-associated protein	223	2e-58
	AAA36415.1	pancreatitis associated protein	221	8e-58
	XP 059401.1	similar to pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein	219	3e-57
U3/C-HI3.48	NP 006735.1	RBP4 gene product	343	1e-94
Mm.2605	VAHU	plasma retinol-binding protein precursor [validated]	343	1e-94
	CAA24959.1	precursor RBP	343	1e-94
	P02753	RETB HUMAN Plasma retinol-binding protein precursor (PRBP) (RBP) (PRO2222)	341	9e-94
	AAH20633.1	Similar to retinol binding protein 4, plasma	341	9e-94
	IRBP	Retinol Binding Protein	340	2e-93
	IBRP	Retinol Binding Protein (Holo Form)	340	2e-93
	IBRQ	Retinol Binding Protein (Apo Form)	340	2e-93
	I401251A	retinol binding protein..	340	2e-93
	IQAB	B Chain E, The Structure Of Human Retinol Binding Protein With Its Carrier Protein Transferrin Reveals Interaction With The Carboxy Terminus Of Rbp	328	8e-90

			IQAB	F Chain F, The Structure Of Human Retinol Binding Protein With Its Carrier Protein Transferrin Reveals Interaction With The Carboxy Terminus Of Rbp		328	8e-90
			AAF69622.1	AF119917 30 P020222		288	5e-78
			CAA2653.1	RBP		199	4e-51
NM_025895							
NP_080171.1		U:(C-HD)4.12	AA038612.1	unknown		298	6e-81
			AAK32724.1	tumor angiogenesis marker		298	6e-81
			AAH11936.1	hypothetical protein DKFZp434N185		298	6e-81
			AAI26906.1	AF318039 1 FKSG20		298	6e-81
			NP_079481.1	endothelial-derived gene 1		274	2e-76
			AAK11563.1	tumor-related protein		274	2e-76
NM_031162		U:(C-D)4.1		CD3Z_HUMAN T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor T3 zeta chain)		233	3e-61
NP_112439.1	Mm.1224	U:(C-HD)2.79	P20963	CD3Z antigen zeta polypeptide (T1T3 complex)		233	3e-61
			AAH25703.1	T-cell receptor zeta chain precursor		228	2e-59
			A31768	T-cell receptor zeta chain		228	2e-59
			AAA60394.1	T-cell receptor zeta chain precursor		227	3e-59
			NP_000725.1	T-cell receptor zeta chain precursor		213	4e-55
			AAF34793.1	AF228312 1 T-cell receptor zeta chain precursor			
NM_008745							
NP_032771.1	Mm.3993	U:(C-HD)3.14	I73631	brain-derived neurotrophic factor receptor precursor, short splice form - human		868	0
			CAA53571.1	protein-tyrosine kinase precursor		868	0
			AAB33110.1	trkB		868	0
			AAH31835.1	Unknown (protein for MGC24881)		868	0
			AAM77876.1	AF508964 1 protein tyrosine kinase non catalytic form		868	0
			NP_006171.2	neurotrophic tyrosine kinase, receptor, type 2		846	0
			AAI67965.1	AF410899 1 neurotrophin receptor tyrosine kinase type 2		846	0
			AAI67967.1	AF410901 1 neurotrophin receptor tyrosine kinase type 2 truncated isoform		846	0

	AA167966.1	AF410900	1 neurotrophin receptor tyrosine kinase type 2 truncated isoform	845	0
	Q16620	TRKB_HUMAN	BDNF/NT-3 growth factors receptor precursor (TrkB tyrosine kinase) (GPI45-TrkB) (Trk-B)	845	0
	A56853		brain-derived neurotrophic factor receptor precursor	845	0
	AA051371.1		tyrosine kinase receptor p145TRK-B	845	0
	AA033109.1		trkB	845	0
	AA092490.1	AF400441	1 neurotrophic tyrosine kinase receptor type 2	845	0
	2103287A		trkB gene	845	0
	AA013693.1		Unknown (protein for MGC:17113)	273	1e-72
	I75633		gene trkC protein	273	1e-72
	AA033112.1		trkC	273	1e-72
	NP_002521.1		neurotrophic tyrosine kinase, receptor, type 3	273	1e-72
	A55178		neurotrophin receptor trkC precursor	273	1e-72
	AAA75374.1		TrkC	273	1e-72
	CAAL2029.1		TRKC	273	1e-72
	Q16288		TRKC_HUMAN NT-3 growth factor receptor precursor (TrkC tyrosine kinase) (GPI45-TrkC)	273	1e-72
	I75632		neurotrophin-3 receptor precursor	273	1e-72
	AA033111.1		trkC	273	1e-72
	2103287B		trkC gene	273	1e-72
	U:(C-D)3.53		Fc fragment of IgG: receptor, transporter, alpha _{1b}	401	e-111
NM_010189	NP_004098.1		FCGN_HUMAN IgG receptor FcRN large subunit P51 precursor (FcRN) (Neonatal Fc receptor)	401	e-111
	P55899		(IgG Fc fragment receptor transporter, alpha chain)	401	e-111
	I38720		hFcRn	401	e-111
	AA058958.1		hFcRn	401	e-111
	AA0108734.1		Fc fragment of IgG: receptor, transporter, alpha	401	e-111

		AAF72596.1	FeRN protein	398 e-111
		AAAG31421.1	AF200220 1 FeRN alpha chain	398 e-110
		1EXU	A Chain A, Crystal Structure Of The Human Mito-Related Fe Receptor	367 e-101
AK015750			A Chain A, Crystal Structure Of Human Estrogen Sulfoltransferase V269e Mutant In The Presence Of Paps	
BAB29956.1	Mem.89655	1HY3	B Chain B, Crystal Structure Of Human Estrogen Sulfoltransferase V269e Mutant In The Presence Of Paps	497 e-140
		1HY3	NP_005411.1	497 e-140
			sulfoltransferase, estrogen-prefering; estrogen sulfoltransferase	494 e-139
		P49888	SUOB HUMAN Estrogen sulfoltransferase (Sulfoltransferase, estrogen-prefering) (EST-1)	494 e-139
		IC2229	estrogen sulfoltransferase (EC 2.8.2.-)	494 e-139
		AAA82125.1	estrogen sulfoltransferase	494 e-139
		AAAB34601.1	estrogen sulfoltransferase; bEST-1	494 e-139
		AAAC50286.1	estrogen sulfoltransferase	494 e-139
		CAA72079.1	estrogen sulfoltransferase	494 e-139
		AAH27956.1	sulfoltransferase, estrogen-prefering	492 e-139
		AAAB65154.1	thyroid hormone sulfoltransferase	323 4e-88
		IC5885	thyroid hormone sulfoltransferase (EC 2.8.2.-) B2	323 4e-88
		BAA24547.1	STIB2	323 4e-88
		AAHI0895.1	Unknown (protein for MGC:13356)	322 9e-88
		IC2523	aryl sulfoltransferase (EC 2.8.2.1) brain isoform	315 1e-85
		AAA67895.1	phenol sulfoltransferase	315 1e-85
		P50225	SUP1 HUMAN Phenol-sulfating phenol sulfoltransferase 1 (p-PST) (Thermosiable phenol sulfoltransferase) (Te-PST) (HAATI/HAAT2) (STIA3)	313 2e-85
		S52794	aryl sulfoltransferase (EC 2.8.2.1)	313 2e-85
		CAA55089.1	aryl sulfoltransferase	313 2e-85
		CAA07495.1	phenol sulfoltransferase	313 2e-85
		2021280C	aryl sulfoltransferase	313 2e-85

			SS2791	aryl sulfotransferase (EC 2.8.2.1)		313	4e-85
			AAB31316.1	aryl sulfotransferase ST1A2		313	4e-85
			CAA55088.1	aryl sulfotransferase		313	4e-85
			2021280B	aryl sulfotransferase		313	4e-85
			157945	phenol-sulfating phenol sulfotransferase		313	4e-85
			AAA99892.1	phenol-sulfating phenol sulfotransferase		313	4e-85
			AAC50480.1	phenol sulfotransferase		313	4e-85
NM_026189		U1(C-D)3.66	BAB21797.1	KIAA1706 protein		103	
NP_080465.2	Mm.6825	U1(C-H)2.51				0	0
			NP_085139.1	KIAA1706 protein		103	0
			BAB55076.1	unnamed protein product		103	0
NM_007669			154380	cyclin-dependent kinase		249	4e-66
NP_031695.1	Mm.34446	U1(C-D)3.6	AAB59559.1	cyclin-dependent kinase		249	4e-66
			AAH01935.1	cyclin-dependent kinase inhibitor 1A (p21, Cyp1)		249	4e-66
			AAH13967.1	cyclin-dependent kinase inhibitor 1A (p21, Cyp1)		249	4e-66
			168674	cyclin-dependent kinase		246	2e-65
			AAB59560.1	cyclin-dependent kinase		246	2e-65
			NP_000380.1	cyclin-dependent kinase inhibitor 1A; melanoma differentiation associated protein 6; CDK-interaction protein 1; wild-type p53-activated fragment 1; DNA synthesis inhibitor		246	2e-65
			NP_510867.1	cyclin-dependent kinase inhibitor 1A; melanoma differentiation associated protein 6; CDK-interaction protein 1; wild-type p53-activated fragment 1; DNA synthesis inhibitor		246	2e-65
			P38936	CDN1 HUMAN Cyclin-dependent kinase inhibitor 1 (p21) (CDK-interacting protein 1)		246	2e-65
			AA004313.1	(Melanoma differentiation associated protein 6) (MDA-6)		246	2e-65
			AAA16109.1	wild type p53 activated fragment-1		246	2e-65
				cyclin-dependent kinase inhibitor		246	2e-65

		AAA19811.1	putative DNA synthesis inhibitor	246	2e-65
		AA329246.1	p21	246	2e-65
		AAA85641.1	alternate gene name=WAF1	246	2e-65
		AAH00275.1	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	246	2e-65
		AAH00312.1	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	246	2e-65
		AAH11787.1	AF497972 1 cyclin-dependent kinase inhibitor 1A (p21, Cip1)	246	2e-65
		2002363A	cyclin kinase inhibitor p21	246	2e-65
		AA615411.1	cyclin-dependent kinase inhibitor isoform	216	4e-56
AK008108		CAC17695.1	dH040G16.1.1 (KIAA1247 (similar to glucosamine-6-sulfatases and KIAA1077), isoform 1)	650	0
BAB25464.1	Mm.35807	XP_030036.1	similar to extracellular sulfatase SULF-1; expressed sequence AW121680	650	0
		AAH76861.1	extracellular sulfatase SULF-2	650	0
		BAA86561.2	KIAA1247 protein	650	0
		XP_053496.2	similar to sulfatase FP	379	e-105
		AAH76860.1	extracellular sulfatase SULF-1	379	e-105
		AAO33315.1	sulfatase SULF1 precursor	379	e-105
		BAC11258.1	unnamed protein product	379	e-105
		BAA83029.1	KIAA1077 protein	379	e-105
		CAB61349.1	hypothetical protein	324	2e-88
		AAH20962.1	similar to glucosamine-6-sulfatases	324	2e-88
		CAC17694.1	dH040G16.1.2 (KIAA1247 (similar to glucosamine-6-sulfatases and KIAA1077), isoform 2)	256	7e-68
		P29992	GB11 HUMAN Guanine nucleotide-binding protein G(Y), alpha subunit (Alpha-11)	706	0
		AAO25615.1	GB11 HUMAN; GUANINE NUCLEOTIDE-BINDING PROTEIN G(Y), ALPHA SUBUNIT; ALPHA-11	706	0
		AAH12614.1	AF493900 1 guanine nucleotide binding protein alpha 11	706	0
NN_010301					
NP_034431.1	Mm.989				

[illegible][illegible]

			AAA59581.1	metalloproteinase inhibitor precursor	422	e-118
			AAA61186.1	metalloproteinase-2 inhibitor precursor	422	e-118
			AAC50729.1	tissue inhibitor of metalloproteinases-2	422	e-118
			IBR9	Human Tissue Inhibitor Of Metalloproteinase-2	411	e-114
			IGXD	C Chain C, Prommp-2/TIMP-2 Complex	411	e-114
			IGXD	D Chain D, Prommp-2/TIMP-2 Complex	411	e-114
			CAA38400.1	Tissue inhibitor of metalloproteinases, Type-2	389	e-108
			AAB24785.1	TIMP-2, CSC-2 IK=tissue inhibitor of metalloproteinase	387	e-107
			2TIMP	N-Terminal Domain Of Tissue Inhibitor Of Metalloproteinase-2 (N-Timp-2), Nurr, 49 Structures	258	2e-68
			NP_003247.1	tissue inhibitor of metalloproteinase 4 precursor	221	2e-57
			Q99727	TM4 HUMAN Metalloproteinase inhibitor 4 precursor (TIMP-4) (Tissue inhibitor of metalloproteinases-4)	221	2e-57
			AAB40391.1	tissue inhibitor of metalloproteinase 4	221	2e-57
			AAC34422.1	tissue inhibitor of metalloproteinase 4	221	2e-57
			AAH10553.1	tissue inhibitor of metalloproteinase 4	221	2e-57
			NP_003109.1	secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (secreted protein, acidic, cysteine-rich)	575	e-163
NM_009242			P09486	SPRC HUMAN SPARC precursor (Secreted protein acidic and rich in cysteine) (Osteonectin) (ON) (Basement membrane protein BM-40)	575	e-163
NP_033268.1		U:(C-D)3:49	GEHUN	osteonectin precursor	575	e-163
			CAA68724.1	extracellular matrix protein BM-40 (AA 1 - 303)	575	e-163
			AAA60570.1	osteonectin	575	e-163
			AAH04974.1	secreted protein, acidic, cysteine-rich (osteonectin)	575	e-163
			AAH08011.1	secreted protein, acidic, cysteine-rich (osteonectin)	575	e-163
			AAA60993.1	osteonectin	573	e-163
			1BMO	A Chain A, Bm-40, F5EC DOMAIN PAIR	496	e-140
			1BMO	B Chain B, Bm-40, F5EC DOMAIN PAIR	496	e-140

						A Chain A, Helix G Deletion Mutant Of Bm-40 Fe-Ec Domain Pair	INUB	474	e-133
						B Chain B, Helix C Deletion Mutant Of Bm-40 Fe-Ec Domain Pair	INUB	474	e-133
						Unknown (protein for MGC:45264)	AAH33721.1	320	5e-87
						SPARC-like 1; masf9, hevfn	NP_004675.2	320	5e-87
						Hvfn-like protein	CAG60386.1	320	5e-87
						SPL1 HUMAN SPARC-like protein 1 precursor (High endothelial venule protein) (Hevfn)	Q14515 (MAST 9)	320	5e-87
						hevin precursor	S60062	320	5e-87
						hevin	CAA57650.1	320	5e-87
						Extracellular Matrix Protein Mod_id: 1; Molecule: Spare; Chain: Null; Fragment: Carboxy-Terminal Domain (Residues 136 - 286); Synonym: Bm-40, Osteonectin, Engineered: Yes; Heterogen: 2 Ca 2+ Ions, One Unidentified Metal Ion Modeled As Ca 2+; Other_details: Crystallized From 0.7 M K ₂ Na-Tartrate, pH 7.5 + 2 mM CaCl ₂	ISRA	311	2e-84
NM_023707						mesotrypsin preproprotein, trypsin 4, brain, protease, serine, 4; mesotrypsinogen, trypsin 3; brain trypsinogen; pancreatic trypsinogen III	NP_002762.2	337	1e-92
NP_076196.1	Mm.46246					mesotrypsinogen	BAA08257.1	337	1e-92
						mesotrypsinogen	AAC13322.1	337	1e-92
						trypsin (EC 3.4.21.4) III precursor	S12764	333	2e-91
						prepro-polypeptide (AA-13 to 234)	CAA3527.1	333	2e-91
						Unknown (protein for IMAGE:4537998)	AAH30238.1	328	3e-90
						trypsinogen IV a-form	CAB58178.1	328	3e-90
						TRY3 HUMAN Trypsin III precursor (Brain trypsinogen) (Trypsin IV)	P95030	328	3e-90
						trypsin (EC 3.4.21.4) IV form a	S23496	328	3e-90
						protease, serine, 1 preproprotein; cationic trypsinogen; trypsinogen A; trypsinogen I; trypsin I; trypsin I	NP_002760.1	327	8e-90
						TRY1 HUMAN Trypsin I precursor (Cationic trypsinogen)	P07477	327	8e-90
						trypsin (EC 3.4.21.4) I precursor	A25852	327	8e-90
						trypsinogen	AAA61231.1	327	8e-90

			AAC80207.1	trypsinogen A	327	8e-90
			I205235A	trypsinogen I	327	8e-90
			AAC80208.1	trypsinogen C	327	1e-89
			NP_002761.1	protease, serine, 2 preproprotein; trypsinogen 2; anionic trypsinogen; trypsin 2; trypsin II	325	3e-89
			P07478	TRY2_HUMAN Trypsin II precursor (Anionic trypsinogen)	325	3e-89
			B25852	trypsin (EC 3.4.21.4) II precursor	325	3e-89
			AAA61232.1	trypsinogen	325	3e-89
			AAC80209.1	trypsinogen E	325	3e-89
			AAC13351.1	anionic trypsinogen	325	3e-89
			I205235B	trypsinogen II	325	3e-89
			I38363	trypsin (EC 3.4.21.4) IV form b precursor	324	6e-89
			2004280A	trypsinogen IV	324	6e-89
			CAA50484.1	trypsinogen IV b-form	324	6e-89
NM_016850						
NP_058546.1	Mm.3233	U:(C-D)3.42	NP_004020.1	interferon regulatory factor 7 isoform b	506	e-143
		U:(C-H)3.17	AAB80688.1	interferon regulatory factor 7B	506	e-143
			NP_001563.2	interferon regulatory factor 7 isoform a	505	e-143
			AAB80686.1	interferon regulatory factor 7A	505	e-143
			Q92985	IRF7_HUMAN Interferon regulatory factor 7 (IRF-7)	505	e-143
			AAB17190.1	interferon regulatory factor 7	505	e-143
			NP_004022.1	interferon regulatory factor 7 isoform d	503	e-142
			AAC70999.1	interferon regulatory factor 7H	503	e-142
			AAB80691.1	putative interferon regulatory factor 7C.2	256	5e-68
NM_009799						
NP_033929.1	Mm.3471	U:(C-D)3.38	NP_001729.1	carbonic anhydrase I; carbonic dehydratase	426	e-119
			P00915	CAHI_HUMAN Carbonic anhydrase I (Carbonate dehydratase I) (CA-I) (Carbonic anhydrase B)	426	e-119
			CRHU1	carbonate dehydratase (EC 4.2.1.1) I	426	e-119

CAA28663.1	carbonic anhydrase I (AA 1-261)	426	e-119
AAA51910.1	carbonic anhydrase I	426	e-119
AAH27890.1	carbonic anhydrase I	426	e-119
1AZM	Drug-Protein Interactions: Structure Of Sulfonamide Drug Complexed With Human Carbonic Anhydrase I	424	e-118
1BZM	Drug-Protein Interactions: Structure Of Sulfonamide Drug Complexed With Human Carbonic Anhydrase I	424	e-118
1CZM	Drug-Protein Interactions: Structure Of Sulfonamide Drug Complexed With Human Carbonic Anhydrase I	424	e-118
1HCB	Carbonic Anhydrase I (E.C.4.2.1.1) Complexed With Bicarbonate	424	e-118
1HUG	Carbonic Anhydrase I (E.C.4.2.1.1) Complexed With Gold Cyanide Inhibitor	424	e-118
1HUH	Carbonic Anhydrase I (E.C.4.2.1.1) Complexed With Iodide Inhibitor	424	e-118
1CRM	Carbonic Anhydrase I (Carbonate Dehydratase I, Hca I) (E.C.4.2.1.1) Complexed With Mercuric Chloride	422	e-118
2CAB	Carbonic Anhydrase Form B (Carbonate Dehydratase) (E.C.4.2.1.1)	422	e-118
1J9W	A Chain A, Solution Structure Of The Cai Michigan 1 Variant	421	e-117
1J9W	B Chain B, Solution Structure Of The Cai Michigan 1 Variant	421	e-117
1JY0	A Chain A, The Crystal Structure Of The Zinc(II) Adduct Of The Cai Michigan 1 Variant	421	e-117
1JY0	B Chain B, The Crystal Structure Of The Zinc(II) Adduct Of The Cai Michigan 1 Variant	421	e-117
BAC04528.1	unnamed protein product	328	7e-90
1BIC	Carbonic Anhydrase II (E.C.4.2.1.1) Mutant With The 200 Replaced By His (T200H) Complex With Bicarbonate	307	2e-83
1205233A	anhydrase, carbonic	305	6e-83
P07451	CAH3 HUMAN Carbonic anhydrase III (Carbonate dehydratase III) (CA-III)	305	6e-83
AAH04897.1	carbonic anhydrase III, muscle specific	305	6e-83
NP_005172.1	carbonic anhydrase III	305	8e-83
CRH03	carbonate dehydratase (EC 4.2.1.1) III	305	8e-83
AAA52293.1	carbonic anhydrase III	305	8e-83

NM_030719 NP_109644.1	Mm.160250	U:(C-D)3.36 U:(C-HD)2.93	AAH21927.1	Unknown (protein for MGC:31979) match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), T59198 (NID:g661035), and AA027979 (NID:g1494038)	399 e-111
			AAC23433.1	unnamed protein product	396 e-110
			BAB70963.1	unnamed protein product	385 e-106
			BAC03870.1	unnamed protein product	210 1e-58
NM_010056 NP_034186.1	Mm.4873	U:(C-D)3.32	NP_005212.1	distal-less homeo box 5	294 e-141
			P56178	DLX5_HUMAN Homeobox protein DLX-5	294 e-141
			AAC17833.1	Dlx-5	294 e-141
			BAB14587.1	unnamed protein product	294 e-141
			AAH06226.1	distal-less homeo box 5	294 e-141
NM_023633 NP_076122.1	Mm.31244	U:(C-D)3.27	NP_078920.1	hypothetical protein FLJ21802	894 0
			BAB15138.1	unnamed protein product	894 0
			AAH11350.1	hypothetical protein FLJ21802	894 0
			BAC16337.1	Mina53	214 3e-55
			AAH14928.1	hypothetical protein FLJ14393	214 5e-55
			NP_116167.3	myc-induced nuclear antigen, 53 kDa isoform 2; Mina53	213 9e-55
			BAC16358.1	Mina53 form-2	213 9e-55
			BAB55024.1	unnamed protein product	210 8e-54
NM_013685 NP_038713.1	Mm.4269	U:(C-D)3.27	NP_003190.1	transcription factor 4 isoform b; Transcription factor 4 (immunoglobulin transcription factor-2)	113 7 0
			P15884	ITF2_HUMAN Transcription factor 4 (immunoglobulin transcription factor 2) (ITF-2) (SL3-3 enhancer factor 2) (SEF-2)	113 7 0
			A41311	transcription factor ITF-2	113 7 0
			AAA60311.1	SEF2-1B protein	113 7 0

	CAA36298.1	ITF-2 DNA binding protein	103	0
	AAA60310.1	SEF2-1A protein	785	0
	NP_003196.1	transcription factor 12	704	0
	Q99081	ITF4 HUMAN TRANSCRIPTION FACTOR 12 (TRANSCRIPTION FACTOR ITF-4)	704	0
	A42121	(E-BOX-BINDING PROTEIN) (DNA-BINDING PROTEIN ITF4)	704	0
	AAA58632.1	transcription factor ITF4	704	0
	AAA58632.1	helix-loop-helix protein	704	0
	AAB62389.1	transcription factor	704	0
	AAH31056.1	transcription factor 4	693	0
	NP_003191.1	transcription factor 3; transcription factor E2-alpha; E2A immunoglobulin enhancer-binding factor E12/E47; immunoglobulin transcription factor 1; kappa-E2-binding factor	512	e-144
	P15923	ITF2 HUMAN Transcription factor E2-alpha (Immunoglobulin enhancer binding factor E12/E47) (Transcription factor-3) (TCF-3) (Immunoglobulin transcription factor-1)	512	e-144
	A34734	(Transcription factor ITF-1) (Kappa-E2-binding factor)	512	e-144
	AAA61146.1	transcription factor 3	512	e-144
	AAA61146.1	transcription factor E2A	512	e-144
	AAA52331.1	e12 protein	506	e-143
	AAC27373.1	ITF2_HUMAN; IMMUNOGLOBULIN ENHANCER BINDING; TRANSCRIPTION FACTOR-3; TCF-3; TRANSCRIPTION FACTOR ITF-1	454	e-127
	S10099	transcription factor ITF-1	409	e-113
	CAA36297.1	ITF-1 DNA binding protein	409	e-113
	AAA58445.1	E2A/HLF fusion protein	345	3c-94
NM_009751	NP_003388.1	flensin; lens intermediate filament protein; LIF-H	694	0
		flensin; cytoskeletal protein, 115 KD	692	0
		BFS1_HUMAN Flensin (Beaded filament structural protein 1) (Lens fiber cell beaded-filament structural protein CP 115) (CP115) (Lens intermediate filament like-heavy) (LIFL-H)	692	0
		flensin	692	0

			CAB89430.1	d531H16.3 (beaded filament structural protein 1, flensin)	692	0
			AAH41483.1	Similar to beaded filament structural protein 1, flensin	585	e-167
			CAA76349.1	flensin	499	e-148
AK017767			NP_060780.2	NA polymerase III transcription initiation factor BRP2; RNA polymerase III transcription initiation factor BRFU; transcription factor IIB-related factor, TFIIB50	476	e-171
NP_079962.1	Mm.87046	U(C-D)3.23	AAAG30222.1	AF298153_1 RNA polymerase III transcription initiation factor BRFU	476	e-171
			AAH10648.1	Unknown (protein for MGC-9916)	476	e-171
			AAAG35669.2	AF206673_1 TFIIB50	476	e-171
			BAA91975.1	unnamed protein product	473	e-170
NM_008093			NP_536721.1	GATA binding protein 5; transcription factor GATA-5; GATA binding factor-5	505	e-142
NP_032119.1	Mm.2527	U(C-D)3.23	Q9BW55	GAT5 HUMAN Transcription factor GATA-5 (GATA binding factor-5)	505	e-142
			CAC36001.1	hb379024.1 (novel protein similar to transcription factor GATA-5)	505	e-142
			NP_005248.1	GATA binding protein 6; GATA-binding protein 6	271	4e-72
			Q92908	GAT6 HUMAN Transcription factor GATA-6 (GATA binding factor-6)	271	4e-72
			AAC50941.1	hGATA-6	271	4e-72
			BAA22621.1	GATA-6	271	4e-72
			CAG64997.1	GATA-6 DNA binding protein	271	4e-72
			NP_002043.1	GATA binding protein 4; GATA-binding protein 4	253	2e-66
			P43694	GAT4_HUMAN Transcription factor GATA-4 (GATA binding factor-4)	253	2e-66
			AAA58496.1	putative	253	2e-66
			I57561	transcription factor GATA-4	243	1e-63
			BAA11334.1	GATA-4 transcription factor	243	1e-63
NM_010286			Q99576	GLZ_HUMAN Glucocorticoid-induced leucine zipper protein (Delta sleep-inducing peptide immunoreactor) (DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-like protein) (TSC-22R)	196	7e-50
NP_034416.1	Mm.22216	U(C-D)3.21 U(C-H)3.22	AAD41085.1	AF153603_1 TSC-22 related protein	196	7e-50

			AF183393_1 TSC-22-like Protein		196	7e-50
			AAG12456.1 glucocorticoid-induced GILZ		196	7e-50
			BAB18680.1 GILZ		196	7e-50
NM_031388					420	e-117
NP_113565.1	Mm.193028	U:(C-D)3.08	NP_114113.1 ubiquitin-specific protease 26		420	e-117
			UBPQ_HUMAN Ubiquitin carboxyl-terminal hydrolase 26 (Ubiquitin thiolesterase 26)		420	e-117
			(Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26)		420	e-117
			AAK31972.1 AF285593_1 ubiquitin specific protease 26		420	e-117
			ubiquitin-specific processing protease; likely ortholog of mouse ubiquitin-specific processing protease 29		327	6e-89
			NP_065954.1		327	6e-89
			Q9HB37 UBPT_HUMAN Ubiquitin carboxyl-terminal hydrolase 29 (Ubiquitin thiolesterase 29)		327	6e-89
			AAG10401.1 AF229438_1 ubiquitin-specific processing protease		327	6e-89
			XP_050754.5 similar to KIAA1594 protein		280	1e-74
			BAB13420.1 KIAA1594 protein		259	1e-68
NM_029796		U:(C-D)3.16			330	3e-90
NP_084072.1	Mm.176946	U:(C-H)2.6	leucine-rich alpha-2-glycoprotein		330	3e-90
			A2GL_HUMAN Leucine-rich alpha-2-glycoprotein precursor (LRG)		330	3e-90
			AAK95527.1 AF403428_1 leucine-rich alpha-2-glycoprotein		330	3e-90
			NBHUA2 leucine-rich alpha-2-glycoprotein		329	6e-90
			AAHB4389.1 leucine-rich alpha-2-glycoprotein		327	2e-89
					112	
NM_007897					3	0
NP_031923.1	Mm.4366	U:(C-D)3.15	Unknown (protein for MGC46380)		109	0
			Q9UH73 COE1_HUMAN Transcription factor COE1 (OE-1) (OE-1) (Early B-cell factor)		109	0
			AAF19643.1 early B-cell transcription factor		8	0
					103	
			AAH41178.1 Similar to early B-cell factor 1		4	0

[illegible]

NM_013569 NP_038597.1	Mm.6539	U(C-D)3.09	NP_000229.1	voltage-gated potassium channel, subfamily H, member 2 isoform a; potassium voltage-gated channel, subfamily H, member 2; ether-a-go-go-related potassium channel protein; human eeg-related gene	194 8	0
			Q12809	KCH2 HUMAN Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go related gene potassium channel 1) (H-ERG) (Erg) (Ether-a-go-go related protein 1) (Eag related protein 1) (eag homolog)	194 8	0
			I39465	probable potassium channel subunit	194 8	0
			AAA62473.1	putative potassium channel subunit	194 8	0
			BAA37096.1	a gene responsible for familial long QT syndrome (LQIT2)	194 8	0
			AAL37559.1	AF363636_1 ether-a-go-go-related K ⁺ channel protein	194 8	0
			AAN05415.1	ether-a-go-go related potassium channel	188 2	0
			CAA09232.1	ether-a-go-go-related protein	181 0	0
			NP_742053.1	voltage-gated potassium channel, subfamily H, member 2 isoform b; potassium voltage-gated channel, subfamily H, member 2; ether-a-go-go-related potassium channel protein; human eeg-related gene	147 6	0
			BAB19682.1	HERG-USO	147 3	0
			NP_742054.1	voltage-gated potassium channel, subfamily H, member 2 isoform c; potassium voltage-gated channel, subfamily H, member 2; ether-a-go-go-related potassium channel protein; human eeg-related gene	128 3	0
			CAD54447.1	potassium channel 1b protein	128 3	0
			AAH01914.1	Similar to potassium voltage-gated channel, subfamily H (eag-related), member 2	117 5	0

[illegible]

AF064749 AAC23667.1	Mm.7562	U:(C-D)3.02	NP_476506.1	alpha 3 type VI collagen isoform 3 precursor; collagen VI, alpha-3 polypeptide	228	9	0
			NP_004360.1	alpha 3 type VI collagen isoform 1 precursor; collagen VI, alpha-3 polypeptide	211	9	0
			P12111	CA36_HUMAN Collagen alpha 3(VI) chain precursor	211	9	0
			CGHU3A	collagen alpha 3(VI) chain precursor	211	9	0
			CAA36267.1	collagen type VI, alpha 3 chain	211	9	0
			NP_476507.1	alpha 3 type VI collagen isoform 4 precursor; collagen VI, alpha-3 polypeptide	211	9	0
			NP_476508.1	alpha 3 type VI collagen isoform 5 precursor; collagen VI, alpha-3 polypeptide	211	9	0
			NP_476505.1	alpha 3 type VI collagen isoform 2 precursor; collagen VI, alpha-3 polypeptide	156	5	0
			AAH33174.1	Similar to collagen, type VI, alpha 3	978	0	0
NM_025725 NP_380001.1	Mm.42368	U:(C-H)3.01	NP_699207.1	hypothetical protein FLJ90575	577	e-164	
			BAC11373.1	unnamed protein product	577	e-164	
NM_007643 NP_031669.1	Mm.18628	U:(C-H)2.65	P16671	CD36_HUMAN Platelet glycoprotein IV (GPIV) (GPIIB) (CD36 antigen) (PAS-4 protein)	798	0	
			A54870	cell adhesion receptor CD36	798	0	
			AAA35534.1	CD36 antigen	798	0	
			AAA58412.1	antigen CD36	798	0	
			AAA58413.1	antigen CD36	798	0	
			CAA83462.1	CD36	798	0	
			AAH08406.1	CD36 antigen (collagen type I receptor, thrombospondin receptor)	798	0	
			2015209A	85kD protein	798	0	

[illegible]

Q06520	SURHA_HUMAN Alcohol sulfotransferase (Hydroxysteroid Sulfotransferase) (HST) (Dehydroepiandrosterone sulfotransferase) (DHEA-ST) (ST2) (ST2A3)	218	2e-56
I38548	alcohol sulfotransferase (EC 2.8.2.2)	218	2e-56
AAA17749.1	dehydroepiandrosterone sulfotransferase	218	2e-56
AAA17750.1	dehydroepiandrosterone sulfotransferase	218	2e-56
CAA59274.1	alcohol sulfotransferase; hydroxysteroid sulfotransferase	218	2e-56
AAC51353.1	dehydroepiandrosterone sulfotransferase	218	2e-56
AAA75491.1	dehydroepiandrosterone sulfotransferase	218	2e-56
AAH20755.1	Unknown (protein for MGC:22602)	218	2e-56
2021281A	dehydroepiandrosterone sulfotransferase	218	2e-56
1EFH	A Chain A, Crystal Structure Of The Human Hydroxysteroid Sulfotransferase In The Presence Of Pap	218	2e-56
1EFH	B Chain B, Crystal Structure Of The Human Hydroxysteroid Sulfotransferase In The Presence Of Pap	218	2e-56
AAA35758.1	dehydroepiandrosterone sulfotransferase	217	2e-56
CAA49755.1	dehydroepiandrosterone sulfotransferase	217	2e-56
AAB23169.2	alcohol/hydroxysteroid sulfotransferase; hSTa	217	2e-56
AAC9987.1	aryl sulfotransferase	208	1e-53
	sulfotransferase family, cytosolic, 1A, phenol-prefering, number 2; thermostable phenol sulfotransferase; phenolic-metabolizing (P) form of PST; arylamine sulfotransferase; aryl sulfotransferase; phenol-prefering phenol sulfotransferase2; phenol-sulfating phenol sulfotransferase 2		
NP_001045.1	aryl sulfotransferase	206	4e-53
G01843	aryl sulfotransferase	206	4e-53
AAB09658.1	aryl sulfotransferase	206	4e-53
AAB09758.1	phenol sulfotransferase	206	4e-53
NP_005698.1	programmed cell death 7; apoptosis-related protein ES18	390	e-108
BAC04915.1	unmatured protein product	390	e-108

NM_022882			AAD20241.1	ES18		317	5e-86
NP_075020.1	Mm.158103	U:(C-D)2,97	NP_055461.1	lipin 2		151	0
			Q92539	LPN2_HUMAN Lipin 2		151	0
			BAA13380.1	Similar to Human KIAA0188 protein		151	0
			BAA11505.1	KIAA0188		809	0
			NP_663731.1	lipin 1		805	0
			Q14693	LPN1_HUMAN Lipin 1		805	0
			AAH0637.1	Similar to lipin 1		805	0
			Q9BQK8_2	[Segment 2 of 3] Lipin 3 (Lipin 3-like)		296	8e-80
			CAC36284.1	d1450M14.3 (novel protein similar to KIAA0188, KIAA0249 and yeast SMP2)		296	8e-80
			Q9BQK8_3	[Segment 3 of 3] Lipin 3 (Lipin 3-like)		234	6e-61
NM_010730			NP_000691.1	annexin I; annexin I (lipocortin I); lipocortin I		597	e-171
NP_034860.1	Mm.14860	U:(C-D)2,97	NP_004083	ANNX1_HUMAN Annexin I (Lipocortin I) (Chromobindin 9) (P3.5) (Phospholipase A2 inhibitory protein)		597	e-171
			LUHU	annexin I		597	e-171
			CAA29338.1	lipocortin (AA.1-346)		597	e-171
			AAH01275.1	annexin A1		597	e-171
			AAH35993.1	similar to annexin A1		597	e-171
			1204261A	lipocortin		597	e-171
			IAIN	Annexin I		545	e-155
			NP_004030.1	annexin A2; annexin II; annexin II (lipocortin II); calpactin I, heavy polypeptide (p36); lipocortin II; Annexin II (lipocortin D); annexin II (lipocortin II); calpactin I, heavy polypeptide		337	2e-92
			P07355	ANNX2_HUMAN Annexin II (Lipocortin II) (Calpactin I heavy chain) (Chromobindin 8) (P36) (Protein I) (Placental anticoagulant protein IV) (PAP-IV)		337	2e-92

LUH036	annexin II	337	2e-92
BA00013.1	lipocortin II	337	2e-92
AAH01388.1	annexin A2	337	2e-92
AAH15834.1	annexin A2	337	2e-92
AAH16774.1	annexin A2	337	2e-92
AAH21114.1	annexin A2	337	2e-92
AAH09564.1	annexin A2	336	5e-92
AAH23990.1	annexin A2	335	7e-92
CAB99342.1	hA255A11.8 (novel protein similar to annexin A2 (ANXA2) (lipocortin II, calpactin I heavy chain, chromobindin 8, PAP-IV))	327	2e-89
NP_001148.1	annexin A11; annexin XI; autoantigen, 56-kD; calyculin-associated annexin 50	287	2e-77
NP_665875.1	annexin A11; annexin XI; autoantigen, 56-kD; calyculin-associated annexin 50	287	2e-77
NP_665876.1	annexin A11; annexin XI; autoantigen, 56-kD; calyculin-associated annexin 50	287	2e-77
P50995	ANXB HUMAN Annexin A11 (Annexin XI) (Calyculin-associated annexin 50) (CAP-50) (56 kDa autoantigen)	287	2e-77
A53132	annexin XI	287	2e-77
AAA19734.1	56K autoantigen	287	2e-77
CAB94995.1	annexin A11	287	2e-77
CAB94996.1	annexin A11	287	2e-77
CAB94997.1	annexin A11	287	2e-77
AAH07564.1	annexin A11	287	2e-77
1AXN	Annexin Family Mol. id: 1; Molecule: Annexin Iii; Chain: Null; Engineered: Yes; Other_details: Human Recombinant	285	8e-77
NP_005130.1	annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III, 1,2-cyclic-inositol-phosphate phosphodiesterase, placental anticoagulant protein III, calcineurin 35-alpha)	285	8e-77
P12429	ANX3 HUMAN Annexin III (Placental anticoagulant protein III) (PAP-III) (35-alpha calcineurin)	285	8e-77
LUH03	annexin III	285	8e-77

		IAII	Annexin III Co-Crystallized With Inositol-2-Phosphate	285	8e-77
		AAA52284.1	1,2-cyclic-inositol-phosphate phosphodiesterase	285	8e-77
		AAA59496.1	lipocortin-III	285	8e-77
		AAA16713.1	annexin III	285	8e-77
		AAH00871.1	annexin A3	285	8e-77
		NP_001147.1	annexin VII isoform 1; annexin VII (synexin); synexin	271	1e-72
		P20073	ANX7 HUMAN Annexin A7 (Annexin VII) (Synexin)	271	1e-72
		AAA36616.1	synexin	271	1e-72
		AAH02632.1	annexin A7	271	1e-72
		BAB93492.1	annexin A7	271	1e-72
NM_009616			meltrin-beta/ADAM 19 homologue	144	
NP_03746.1	Mm.89940	CAC20585.1	meltrin-beta/ADAM 19 homologue	0	0
		NP_150377.1	a disintegrin and metalloproteinase domain 19 isoform 2 preproprotein; meltrin beta	144	0
		AAK07852.1	AF311317_1 disintegrin and metalloproteinase ADAM19	144	0
		NP_075525.2	a disintegrin and metalloproteinase domain 19 isoform 1 preproprotein; meltrin beta	142	0
		Q9H013	AD19 HUMAN ADAM 19 precursor (A disintegrin and metalloproteinase domain 19) (Meltrin beta) (Metalloprotease and disintegrin dentritic antigen marker) (MADDAM)	142	0
				6	0
		AAG50282.1	AF326918_1 metalloprotease-disintegrin meltrin beta	142	0
				6	0
		AAF21162.1	AF134707_1 disintegrin and metalloproteinase domain 19	129	0
		AAH33132.1	Unknown (protein for IMAGE3615066)	7	0
		AAH24214.1	Unknown (protein for IMAGE3604198)	741	0
			a disintegrin and metalloprotease domain 12 isoform 1 preproprotein; A disintegrin and metalloproteinase domain 12 (Meltrin-alpha, mouse, homolog of); meltrin alpha	741	0
		NP_003465.2		609	0

			O43184	AD12_HUMAN ADAM 12 precursor (A disintegrin and metalloproteinase domain 12) (Meltrin alpha)	669	0
			AAC08702.2	meltin-L precursor	669	0
			NP_067673.1	a disintegrin and metalloprotease domain 12 isoform 2 preproprotein; A disintegrin and metalloprotease domain 12 (Melnin-alpha, mouse, homolog of); meltrin alpha	669	0
			AAC08703.2	meltin-S	669	0
			NP_001655.1	ras homolog gene family, member A; Aphysia ras-related homolog 12; Rho12; RhoA; Ras homolog gene family, member A (oncogene RHO H12)	335	1e-91
			P06749	RHOA_HUMAN Transforming protein RhoA (H12)	335	1e-91
			TVHU12	GTP-binding protein rhoA	335	1e-91
			CAA28690.1	ORF (AA 1-193)	335	1e-91
			AAC33178.1	GTP-binding protein	335	1e-91
			AAH01360.1	ras homolog gene family, member A	335	1e-91
			AAH05976.1	ras homolog gene family, member A	335	1e-91
			AAM21117.1	AF498970_1 small GTP binding protein RhoA	335	1e-91
			ILB1	B Chain B, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbps In Complex With Rhoa	331	1e-90
			ILB1	D Chain D, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbps In Complex With Rhoa	331	1e-90
			ILB1	JF Chain F, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbps In Complex With Rhoa	331	1e-90
			ILB1	H Chain H, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbps In Complex With Rhoa	331	1e-90
			IFTN	Crystal Structure Of The Human RhoGDP COMPLEX	331	1e-90
			ICCO	A Chain A, Crystal Structure Of The RhoA Gdp-Rhogdi Complex	330	4e-90
			ICCO	C Chain C, Crystal Structure Of The RhoA Gdp-Rhogdi Complex	330	4e-90
			AAA50612.1	multidrug resistance protein	328	1e-89

	NP_786886.1	ras homolog gene family, member C; Aplysia RAS-related homolog 9 (oncogene RHO H9); Aplysia ras-related homolog 9; RhoC; RAS homolog gene family, member C (oncogene RHO H9)	319	7e-87
	P08134	RHOC_HUMAN Transforming protein RhoC (H9)	319	7e-87
	TVEURC	GTP-binding protein rhoC	319	7e-87
	CAA29969.1	rhoC coding region (AA 1-193)	319	7e-87
	AAC33179.1	GTPase	319	7e-87
	AAH07245.1	ras homolog gene family, member C	319	7e-87
	AAH09177.1	ras homolog gene family, member C	319	7e-87
	AAM21119.1	AF498972_1 small GTP binding protein RhoC	319	7e-87
	I42B	Human RhoA Complexed With Gdp Analogue	317	2e-86
	ICXZ	A Chain A, Crystal Structure Of Human RhoA Complexed With The Effector Domain Of The Protein Kinase PknPRK1	317	2e-86
	IDPF	A Chain A, Crystal Structure Of A Mg-Free Form Of RhoA Complexed With Gdp	311	1e-84
		ras homolog gene family, member B; Aplysia RAS-related homolog 6 (oncogene RHO H6); Aplysia ras-related homolog 6; RhoB; RAS homolog gene family, member B (oncogene RHO H6)		
	NP_004031.1		303	4e-82
	P01121	RHOB_HUMAN Transforming protein RhoB (H6)	303	4e-82
	TVEUHH	GTP-binding protein: rhoB - human	303	4e-82
	CAA29968.1	rhoB [Homo sapiens]	303	4e-82
	AAM21118.1	AF498971_1 small GTP binding protein RhoB	303	4e-82
	ITX4	B Chain B, RhoRHOGAPGDP(DOT)/ALF4 COMPLEX	300	3e-81
			141	
	I77349	platelet glycoprotein IIIa precursor	1	0
	AAA35927.1	platelet glycoprotein IIIa (GPIIIa)	141	
			1	0
	AAA52600.1	platelet glycoprotein IIIa	140	-9
				0
NNM_016780 NP_058060.1	Mm.8013	U1-(C-D)2.92		

A60798	platelet glycoprotein IIIa beta chain (version 2)	140	6	0
AAA67537.1	glycoprotein IIIa	140	2	0
NP_000203.1	integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precursor	140	1	0
AAA60122.1	glycoprotein IIIa	140	1	0
P05106	ITB3_HUMAN Integrin beta-3 precursor (Platelet membrane glycoprotein IIIa) (GPIIb) (CD61 antigen)	140	0	0
A26547	platelet glycoprotein IIIa beta chain precursor (version 1)	140	0	0
AAA52589.1	glycoprotein IIIa precursor	140	0	0
B36268	platelet glycoprotein IIIa-II	136	7	0
AAB71380.1	platelet membrane glycoprotein IIIa beta subunit	135	8	0
I1VZ	B Chain B, Crystal Structure Of The Extracellular Segment Of Integrin Alphavbeta3	133	9	0
IL5G	B Chain B, Crystal Structure Of The Extracellular Segment Of Integrin Avb3 In Complex With An Arg-Gly-Asp Ligand	133	9	0
IMIX	B Chain B, Crystal Structure Of The Extracellular Segment Of Integrin Alpha Vbeta3 Bound To Mn2+	133	9	0
AAA52707.1	integrin beta-5 subunit	820		0
NP_002033.1	gamma-aminobutyric acid (GABA) receptor, rho-1	881	0	0
P24046	GABRI_HUMAN Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor)	881	0	0
A38627	gamma-aminobutyric acid receptor A rho-1 chain precursor	881	0	0

AAA52509.1	gamma-aminobutyric acid receptor type A rho-1 subunit	881	0
P28476	GAB2_HUMAN Gamma-aminobutyric-acid receptor rho-2 subunit precursor (GABA(A) receptor)	654	0
CAC07339.1	d1131187.1 (gamma-aminobutyric acid (GABA) receptor rho 2)	654	0
NP_002034.1	gamma-aminobutyric acid (GABA) receptor, rho 2 precursor	652	0
A33079	gamma-aminobutyric acid receptor rho-2 chain precursor	652	0
AAA52510.1	gamma-amino butyric acid	652	0
XP_1160362	similar to Gamma-aminobutyric-acid receptor rho-3 subunit precursor (GABA(A) receptor)	459	e-129
NP_068712.1	gamma-aminobutyric acid (GABA) A receptor, beta 3 isoform 2 precursor	315	2e-85
NP_000805.1	gamma-aminobutyric acid (GABA) A receptor, beta 3 isoform 1 precursor	315	2e-85
P28472	GAB3_HUMAN Gamma-aminobutyric-acid receptor beta-3 subunit precursor (GABA(A) receptor)	315	2e-85
A55275	gamma-aminobutyric acid A receptor beta 3 chain splice form 1	315	2e-85
AAA52511.1	GABA-alpha receptor beta-3 subunit	315	2e-85
AAH10641.1	AAH10641 gamma-aminobutyric acid (GABA) A receptor, beta 3	312	1e-84
NP_000806.1	gamma-aminobutyric acid (GABA) A receptor, delta	305	2e-82
O14764	GAD_HUMAN Gamma-aminobutyric-acid receptor delta subunit precursor (GABA(A) receptor)	305	2e-82
AAB70007.1	GABA-A receptor delta subunit	305	2e-82
AAH33801.1	gamma-aminobutyric acid (GABA) A receptor, delta	302	1e-81
NP_000804.1	gamma-aminobutyric acid (GABA) A receptor, beta 2 isoform 2	302	1e-81
P47870	GAB2_HUMAN Gamma-aminobutyric-acid receptor beta-2 subunit precursor (GABA(A) receptor)	302	1e-81
AAB29370.1	gamma-aminobutyric acid A receptor beta 2 subunit; (GABA)A receptor beta 2 subunit	302	1e-81
AAB33983.1	GABAA receptor beta 2 subunit	302	1e-81
U1(C-D)2.76	soluble mannose-binding lectin precursor; mannose-binding lectin; mannose binding protein; Mannose-binding lectin 2, soluble (opsone defect) [Homo sapiens]	244	1e-64
NP_000233.1	MABC_HUMAN Mannose-binding protein C precursor (MBP-C) (MBP1) (Mannan-binding protein) (Mannose-binding lectin)	244	1e-64

[illegible]

[illegible]

[illegible]

U28789	U:(C-D)2.82	AF352051.1	proliferation potential-related protein	126	0
AA049620.1	U:(C-H)2.79	AA105625.1	hypothetical protein DKFZp61B2423.1	608	e-173
		T50609	hypothetical protein	608	e-173
		CAB94869.1	retinoblastoma-binding protein 6	534	e-151
		NP_008841.1	retinoblastoma-binding protein RBQ-1	534	e-151
		A57640	RB protein binding protein	534	e-151
		CAA59445.1			
NM_010287		BAA96064.1	KIAA1540 protein	687	0
NP_034417.1	U:(C-H)2.82	NP_057624.1	G protein-coupled receptor 72; G-protein coupled receptor	684	0
		Q9NTM4	GP72_HUMAN Probable G protein-coupled receptor GPR72 precursor	684	0
		AA043705.1	AF236081.1 orphan G-protein coupled receptor GPR72	684	0
		CAC19039.1	glucocorticoid induced receptor	199	1e-50
NM_016759		NP_006686.1	Rap2 interacting protein 8	729	0
NP_058039.1	U:(C-D)2.81	AA09366.1	Rap2 interacting protein 8	729	0
		AA06194.1	AAH06194 Rap2 interacting protein 8	729	0
		AA068767.1	Rap2 interacting protein 8	712	0
		T43467	hypothetical protein DKFZp434A1727.1	661	0
		CAB63771.1	hypothetical protein	661	0
		NP_612147.1	Rap2 binding protein 9	422	e-118
		BAB70882.1	unnamed protein product	422	e-118
		AAH22520.1	Unknown (protein for MCC:26655)	362	e-100
		AAK52313.1	Rap2 binding protein 9	308	1e-83
		AA049150.1	AC002457_2 unknown	273	4e-73
AK004851		NP_061821.1	Gene 33/Mig-6	641	0
NP_598514.1	U:(H-D)2.81				

		Q9UIM3	MIG6, HUMAN Mitogen-inducible gene 6 protein (Mig-6)	641	0
		CAC20426.1	mitogen inducible gene mig-6 product	641	0
		AAH25337.1	Gene 33/Mig-6	641	0
		AAB35056.1	Mig-6=mitogen-inducible gene mig-6 product [human, WI-38 cells, Peptide, 462 aa]	635	0
		T46346	hypothetical protein DKFZp434J1114.1	291	4e-78
		CAB70672.1	hypothetical protein	291	4e-78
	U:(C-D)2.81				
NM_023061		AAAI7799.1	cell surface glycoprotein P1H12 precursor	933	0
NP_075548.1	Mm.39103	NP_006491.1	melanoma cell adhesion molecule; melanoma adhesion molecule	926	0
			MUC18, HUMAN Cell surface glycoprotein MUC18 precursor (Melanoma-associated antigen MUC18) (Melanoma-associated antigen A32) (S-endo1 endothelial-associated antigen) (CD146 antigen) (Melanoma adhesion molecule)		
		P43121		926	0
		I38049	cell surface glycoprotein MUC18 precursor	926	0
		AAA20922.1	MUC18 glycoprotein	926	0
		AAA20824.1	MUC18 glycoprotein	926	0
		CAA48332.1	melanoma associated glycoprotein	926	0
		NP_005572.1	Lutheran blood group (Auberg b antigen included); B-cell adhesion molecule; Lutheran blood group; Auberg b blood group	208	4e-53
		P50895	LU_HUMAN Lutheran blood group glycoprotein precursor (B-CAM cell surface glycoprotein) (Auberg B antigen) (F8/G253 antigen)	208	4e-53
		I38000	Lutheran blood group glycoprotein precursor	208	4e-53
		CAA53849.1	Lutheran blood group glycoprotein	208	4e-53
		I37202	B-CAM protein	201	4e-51
		CAA53327.1	B-CAM	201	4e-51
	U:(C-D)2.8				
AF263458		NP_057703.1	placenta-specific 8	210	1e-54
AAF76887.1	Mm.34609	AAF64260.1	AF208846.1 BM-004	210	1e-54
		CAD19530.1	C15 protein	210	1e-54

[illegible]

		IDVN	A Chain A, Latent Form Of Plasminogen Activator Inhibitor-1 (Pai-1)	211	5e-54
		ILJ5	A Chain A, 18a Resolution Structure Of Latent Plasminogen Activator Inhibitor-1 (Pai-1)	211	5e-54
		NP_000593.1	plasminogen activator inhibitor-1; plasminogen activator inhibitor, type I	211	5e-54
		P05121	PAI1, HUMAN Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial plasminogen activator inhibitor) (PAI)	211	5e-54
		I7HUP1	plasminogen activator inhibitor 1 precursor [validated]	211	5e-54
		IC5G	A Chain A, Plasminogen Activator Inhibitor-1	211	5e-54
		CAA28025.1	precursor polypeptide	211	5e-54
		AAA60003.1	plasminogen activator inhibitor-1	211	5e-54
		AAA60007.1	plasminogen activator-1	211	5e-54
		AAD45828.1	AC004876.1 plasminogen activator inhibitor-1 precursor	211	5e-54
		AAK60338.1	AF386492.1 serine-cysteine proteinase inhibitor clade E member 1	211	5e-54
		AAHI0860.1	Serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	211	5e-54
		LA7C	A Chain A, Human Plasminogen Activator Inhibitor Type-1 In Complex With A Pentapeptide	211	6e-54
	U1(C-D)2.72 U1(C-HD)2.8	NP_001164.1	Rho GTPase activating protein 5; RhoGAP5; p190-B	272	0
		B5943.1	Rho GTPase activating protein 5 (p190-B) [imported]	272	0
		AAA95963.1	p190-B	272	0
		NP_077318.1	glucocorticoid receptor DNA binding factor 1 isoform a	138	0
		BAB21813.2	KIAA1722 protein	138	0
		NP_004482.2	glucocorticoid receptor DNA binding factor 1 isoform b	135	0
		AAF80386.1	AF159851.1 Rho GAP p190-A	135	0

			A40971	DNA-binding protein GRF-1	600	e-171
			AA58618.1	glucocorticoid receptor repression factor 1	600	e-171
			XP_210679.1	similar to Rho GTPase activating protein 5 [Mus musculus]	283	1e-75
NM_021301					112	
NP_067276.1	Mm.63479	U:(C-HI)2.8	AAH44572.1	similar to solute carrier family 15 (H+/peptide transporter), member 2	8	0
			NP_066568.1	solute carrier family 15 (H+/peptide transporter), member 2	112	
			Q16348	PET2_HUMAN Oligopeptide transporter, kidney isoform (Peptide transporter 2) (Kidney H+/peptide cotransporter) (Solute carrier family 15, member 2)	112	0
			I52481	PEPT 2	112	0
			AAB34388.1	PEPT 2	112	0
			2113198A	H/peptide cotransporter	112	0
			AAC15477.1	Ctco-2 oligopeptide transporter	561	e-159
			NP_005064.1	solute carrier family 15 (oligopeptide transporter), member 1; peptide transporter HPEPT1	561	e-159
			P46059	PET1_HUMAN Oligopeptide transporter, small intestine isoform (Peptide transporter 1) (Intestinal H+/peptide cotransporter) (Solute carrier family 15, member 1)	561	e-159
			A56163	peptide transport protein hPEPT1	561	e-159
			AAA63797.1	peptide transporter	561	e-159
			AAB61693.1	intestinal H+/peptide cotransporter	561	e-159
			CAC27442.1	ba551M18.1.1 (solute carrier family 15 (oligopeptide transporter) member 1)	502	e-141
			IC5638	pH-sensing regulatory factor	231	4e-60
			BAA22632.1	pH-sensing regulatory factor of peptide transporter	231	4e-60
AK008098						
BAB25458.1	Mm.10706	U:(C-D)2.8	NP_000959.2	ribosomal protein L4; 60S ribosomal protein L4; homologue of Xenopus ribosomal protein L1	659	0
			P36578	RL4_HUMAN 60S ribosomal protein L4 (L1)	659	0
			BAA04887.1	ribosomal protein	659	0

			AAH01365.1	AAH01365 ribosomal protein L4		659	0
			AAH05817.1	AAH05817 ribosomal protein L4		659	0
			AAH07748.1	AAH07748 ribosomal protein L4		659	0
			AAH07996.1	AAH07996 ribosomal protein L4		659	0
			AAH09888.1	AAH09888 ribosomal protein L4		659	0
			AAH10151.1	AAH10151 ribosomal protein L4		659	0
			AAH14653.1	AAH14653 Similar to ribosomal protein L4		659	0
			BAB79458.1	ribosomal protein L4		659	0
			T09551	ribosomal protein L4		646	0
			CAA52154.1	ribosomal protein L4		646	0
			AAA60281.1	ribosomal protein L4		604	e-173
			XP_034640.1	similar to ribosomal protein L4; 60S ribosomal protein L4; homologue of Xenopus ribosomal protein L1		440	e-123
NM_030257			XP_057302.2	similar to cDNA sequence BC003322; hypothetical protein, MGC:7041 [Mus musculus]		476	e-134
NP_084533.1	Mm.155880	U1(C-D)2.79	T46287	hypothetical protein DKFZp727102.1.1		268	3e-71
			CAB70692.1	hypothetical protein		268	3e-71
AK010201		U1(C-D)2.79	NP_057145.1	Yippee protein		248	1e-65
BAB26764.1	Mm.22145	U1(C-H)2.6	Q9Y3C9	YIPPE_HUMAN Yippee homolog (CGI-127)		248	1e-65
			AAD34122.1	AF151885_1 CGI-127 protein		248	1e-65
			AAF43785.1	AF135161_1 unknown		248	1e-65
			AAH00836.1	AAH00836 CGI-127 protein		248	1e-65
			T50836	Yippee protein [imported]		209	7e-54
			AAD47882.1	AF172940_1 Yippee protein		209	7e-54
NM_008344				insulin-like growth factor binding protein 6		306	4e-83
NP_032370.1	Mm.21373	U1(C-D)2.77	AAA88070.1	insulin-like growth factor binding protein 6		306	4e-83

		NP_002169.1	insulin-like growth factor binding protein 6		306	4e-83
		PZ4592	IDP6 HUMAN Insulin-like growth factor binding protein 6 precursor (IGFBP-6) (IBP-6) (IGF-binding protein 6)		306	4e-83
		AJ39842	Insulin-like growth factor-binding protein 6 precursor		306	4e-83
		AAB06187.1	(GF-BP 4		306	4e-83
		CAA07346.1	insulin-like growth factor binding protein 6		306	4e-83
		AAH03507.1	AAH03507 insulin-like growth factor binding protein 6		306	4e-83
		AAH03507.1	AAH03507 insulin-like growth factor binding protein 6		306	4e-83
		AAH10162.1	AAH10162 insulin-like growth factor binding protein 6		306	4e-83
		AAH11708.1	AAH11708 insulin-like growth factor binding protein 6		306	4e-83
		NP_079036.1	hypothetical protein FLJ14009		418 e-116	
	Mm.206764	BAB14815.1	unnamed protein product		418 e-116	
	U:(C-D)2.77	AAH20206.1	AAH20206 hypothetical protein FLJ14009		418 e-116	
		AAD38076.1	AC007766 2 R26610 1		367 e-101	
		NP_036528.1	plectstrin homology-like domain, family A, member 3; plectstrin homology-like domain, family A, member 2		246	5e-65
	Mm.34346	AAD42081.1	AFI51100 1 TDA051/tpl homologue 1		246	5e-65
		AAH14390.1	AAH14390 Similar to plectstrin homology-like domain, family A, member 3		246	5e-65
		BAC11454.1	unnamed protein product		242	8e-64
		NP_002890.1	retinol binding protein 1, cellular; retinol-binding protein 1,		275	2e-73
	U:(C-HD)2.75	cellular			275	2e-73
		P09455	RETI HUMAN Retinol-binding protein I, cellular (Cellular retinol-binding protein) (CRBP)		275	2e-73
		RJUO	retinol-binding protein, cellular		275	2e-73
		AAA60257.1	retinol-binding protein		275	2e-73
		CAA30318.1	cellular retinol binding protein		275	2e-73

NM_019576			AAA35714.1	retinol-binding protein	251	3c-66
NP_062522.1	Mm.32067	U(C-H)2.74	NP_061146.1	TMTSP for transmembrane molecule with thrombospondin module	134	4
			BAA96553.1	transmembrane molecule with thrombospondin module	134	4
NM_026002			AAI92861.1	LYRIC	838	0
NP_080278.2	Mm.196159	U(C-H)2.74	AAH5642.1	LYRIC protein	836	0
NM_009368			NP_003230.1	transforming growth factor, beta 3	766	0
NP_033394.1	Mm.1291	U(C-D)2.72	P10600	TGF3 HUMAN Transforming growth factor beta 3 precursor (TGF-beta 3)	766	0
			A36169	transforming growth factor beta-3 precursor	766	0
			CAA32362.2	TGF-beta 3 (AA 1-412)	766	0
			AAA61161.1	transforming growth factor-beta3	766	0
			AAC79727.1	transforming growth factor-beta 3	766	0
			AAM96819.1	transforming growth factor, beta 3	766	0
			AAO13495.1	transforming growth factor, beta 3	766	0
			CAA33024.1	transforming growth factor-beta 3	762	0
			AAH18503.1	AAH18503 Similar to transforming growth factor, beta 3	542	e-154
			NP_003229.1	transforming growth factor, beta 2	432	e-120
			P08112	TGF2 HUMAN Transforming growth factor beta 2 precursor (TGF-beta 2) (Glioblastoma-derived T-cell suppressor factor) (G-TSF) (BSC-1 cell growth inhibitor) (Polyargin) (Cetermin)	432	e-120
			A31249	transforming growth factor beta-2 precursor, short form	432	e-120
			CAA68279.1	G-Tsf precursor	432	e-120
			AAA50405.1	transforming growth factor beta 2	427	e-119
			B31249	transforming growth factor beta-2 precursor, long form	422	e-117
			AAA50404.1	transforming growth factor-beta-2 precursor	422	e-117

	P0137	TGFI_HUMAN Transforming growth factor beta 1 precursor (TGF-beta 1)	302	1e-81
	WPHU2	transforming growth factor beta-1 precursor [validated]	302	1e-81
	CAL29283.1	transforming growth factor beta 1 precursor	302	1e-81
	AAH00125.1	AAH00125 Similar to transforming growth factor, beta 1	302	1e-81
	AAH01180.1	AAH01180 Similar to transforming growth factor, beta 1	302	1e-81
	AAH2242.1	Unknown (protein for MGC:22008)	302	1e-81
	NP_000651.1	transforming growth factor, beta 1 (Camurati-Engelmann disease); transforming growth factor, beta 1; diaphyseal dysplasia 1, progressive (Camurati-Engelmann disease)	301	4e-81
	CAA26580.1	TGF-beta precursor	301	4e-81
	I109243A	transforming growth factor beta	301	4e-81
	ITGK	Human Transforming Growth Factor Beta 3, Crystallized From Peg 4000	248	3e-65
	ITGI	Human Transforming Growth Factor-Beta 3, Crystallized From Dioxane	248	3e-65
	IKTZ	A Chain A, Crystal Structure Of The Human Tgf-Beta Type II Receptor Extracellular Domain In Complex With Tgf-Beta3	248	3e-65
	ITFG	Transforming Growth Factor Type Beta 2 (Tgf-B2)	210	8e-54
	2TGI	Transforming Growth Factor-Beta Two (Tgf-B2)	210	8e-54
NM_030256 NP_084532.1	XP_208546.1	similar to cDNA sequence BC003321; hypothetical protein, MGC:7014 [Mus musculus]	491	e-138
NM_007617 NP_031643.1	NP_001225.1	caveolin 3; M-caveolin; caveolin-3	305	6e-83
	NP_203123.1	caveolin 3; M-caveolin; caveolin-3	305	6e-83
	P56539	CAV3_HUMAN Caveolin-3 (M-caveolin)	305	6e-83
	CAA75042.1	caveolin 3	305	6e-83
	AAC39756.1	caveolin-3	305	6e-83
	AAC39758.1	caveolin-3	305	6e-83
	AAC14931.1	caveolin-3	303	2e-82
	AAH06432.1	AAH06432 Similar to caveolin 1, caveolae protein, 22kD	218	1e-56

			NP_001744.2	caveolin 1; caveolin 1, caveolae protein, 22kD; caveolae protein, 22-kD; caveolin 1 caveolae protein, 22kD; caveolin 1, alpha isoform; caveolin 1, beta isoform	218	1e-56
			Q03135	CAVI_HUMAN Caveolin-1	218	1e-56
			AAD23745.1	caveolin-1	218	1e-56
			AAH09685.1	AAH09685 Unknwn (protein for MGC:8998)	218	1e-56
			S26884	caveolin	213	3e-55
			CAA79476.1	caveolin	213	3e-55
NM_008107			AAB94786.1	GDF-1	391	e-108
NP_032133.1	Mm.7914	U:(C-D)2.71	NP_001483.2	growth differentiation factor 1	389	e-108
			P27539	GDF1_HUMAN Embryonic growth/differentiation factor 1 precursor (GDF-1)	389	e-108
			C39364	GDF-1 embryonic growth factor	389	e-108
			AAAS8501.1	growth/differentiation factor 1	389	e-108
NM_025684			XP_167042.1	similar to RIKEN cDNA 5730521E12 [Mus musculus]	322	1e-87
NP_079960.1	Mm.90950	U:(C-D)2.7	NP_003170.1	synaptophysin; major synaptic vesicle protein P38	463	e-130
NM_009305			P08247	SYPH_HUMAN Synaptophysin (Major synaptic vesicle protein P38)	463	e-130
NP_033331.1	Mm.2397	U:(C-D)2.7	A35699	synaptophysin	463	e-130
			AAB92358.1	synaptophysin	463	e-130
			AAF03829.1	AF196779_6 synaptophysin	463	e-130
			CAA29686.1	synaptophysin	442	e-124
			NP_653243.1	synaptophysin	282	2e-75
			AAH22518.1	Similar to synaptophysin	282	2e-75
			CAD39117.1	hypothetical protein	282	2e-75
			AAH03681.2	AF411860_1 synaptophysin	282	2e-75
			NP_006745.1	synaptophysin-like protein; panthophysin	201	4e-51

		I53171	pantophysin		201	4e-51
		CAA48276.1	h-Sp		201	4e-51
		AAB31344.1	pantophysin		201	4e-51
		AAD50513.1	AC005095_1 pantophysin		201	4e-51
		AAH16835.1	AAH16835 Similar to syntrophysin-like protein		200	6e-51
		AAH20938.1	AAH20938 Unknown (protein for MGC:24750)		200	6e-51
NM_010434					207	
NP_034564.1	Mm.20333	AAAG25990.1	AF305239_1 Fas-interacting serine/threonine kinase 3		5	0
		AAC64294.1	PKY protein kinase		206	0
		CAC13164.1	dJ8L15.1 (homeodomain-interacting protein kinase 3)		206	0
		AAL37371.1	AF326592_1 homeodomain interacting protein kinase 2		103	0
		Q9H2X6	HIK2 HUMAN Homeodomain-interacting protein kinase 2		102	0
		NP_073377.1	homeodomain interacting protein kinase 2; homeodomain-interacting protein kinase 2		102	0
		AAG41236.1	AF208291_1 protein kinase HIPK2		102	0
		AAG35710.1	AF207702_1 homeodomain-interacting protein kinase 2		885	0
		BAC57075.1	homeodomain-interacting protein kinase-1		827	0
		NP_689509.1	homeodomain-interacting protein kinase 1; homeodomain interacting protein kinase 1-like protein; nuclear body associated kinase 2b		827	0
		AAH33012.1	Similar to homeodomain interacting protein kinase 1		827	0
		CAA70489.1	protein kinase		558	e-158
NM_011775			zona pellucida glycoprotein 2 preproprotein; zona pellucida sperm-binding protein 2 precursor;		810	0
NP_035905.1	Mm.6510	NP_003451.1	zona pellucida protein A			
			U ₁ (C-D)2.7			
			U ₁ (C-D)2.68			

			Q05996	ZP2_HUMAN Zona pellucida sperm-binding protein 2 precursor (Zona pellucida glycoprotein ZP2) (Zona pellucida protein A)	810	0
			A48833	sperm-binding glycoprotein ZP2 precursor	810	0
			AAA61335.1	zona pellucida ZP2 glycoprotein	810	0
			AAB67599.1	zona pellucida ZP2	810	0
	U:(C-D)2.68					
	U:(C-H)2.58		NP_004678.1	myotubularin related protein 4; zinc finger, FYVE domain containing 11	220	0
AF262986						
AAK58180.1	Mm.90390		AAAF72539.1	AF264717_1 FYVE domain-containing dual specificity protein phosphatase FYVE-DSF2	220	0
			BAA31622.2	KIAA0647 protein	220	0
			AAH35609.1	myotubularin related protein 4	220	0
			T00375	hypothetical protein KIAA0647	184	0
			NP_066576.1	myotubularin-related protein 3 isoform c; FYVE (Fab1 YGLO23 Vsp27 BEA1 domain) dual-specificity protein phosphatase; zinc finger, FYVE domain containing 10	105	0
			BAA20826.1	KIAA0371	105	0
			AAF40205.1	AF233438_1 FYVE domain-containing dual specificity protein phosphatase FYVE-DSF1c	105	0
			NP_694691.1	myotubularin-related protein 3 isoform b; FYVE (Fab1 YGLO23 Vsp27 BEA1 domain) dual-specificity protein phosphatase; zinc finger, FYVE domain containing 10	101	0
			AAF40204.1	AF233437_1 FYVE domain-containing dual specificity protein phosphatase FYVE-DSF1b	101	0
			NP_694690.1	myotubularin-related protein 3 isoform a; FYVE (Fab1 YGLO23 Vsp27 BEA1 domain) dual-specificity protein phosphatase; zinc finger, FYVE domain containing 10	100	0
			AAF40203.2	AF233436_1 FYVE domain-containing dual specificity protein phosphatase FYVE-DSF1a	100	0

					AAB833949.1	match to AB002369 [NID:g2224682]	641	0
					AAB88872.1	match to AB002369 [NID:g2224682]	424	e-118
					NP_057240.1	myotubularin-related protein 2	328	4e-89
					QJ3614	MTR2_HUMAN Myotubularin-related protein 2	328	4e-89
					BAA83025.1	KIAA1073 protein	328	4e-89
					NP_000243.1	myotubularin	325	6e-88
					QJ3496	MTM1_HUMAN Myotubularin	325	6e-88
					AAC51682.1	myotubularin	325	6e-88
					AAC12865.1	myotubularin	325	6e-88
					BAA13200.1	similar to a human major CRK-binding protein DOCK180.	341	2
					XP_047961.5	similar to dedicator of cyto-kinesis 2 [Mus musculus]	333	0
					NP_001371.1	dedicator of cyto-kinesis 1	211	3
					BAA09454.1	DOCK180 protein	211	3
					AANI2301.1	modifier of cell adhesion	117	4
					BAA20759.1	KIAA0299	106	3
					AAH41761.1	Similar to dedicator of cyto-kinesis 1	769	0
					T01438	hypothetical protein GS034D21.1	541	e-153
					AB833946.1	60% similar to AB002297 (PID:g2224539)	541	e-153
					BAC03696.1	unnamed protein product	526	e-149
					T01357	hypothetical protein H_GS368F15.1	474	e-133
					XP_209883.1	similar to hypothetical protein E130320D18 [Mus musculus]	419	e-116

NM_018733 NP_061203.1	NULL	U:(C-D)2.68	BAC45228.1	Voltage-gated sodium channel alpha 1 subunit	868	0
			AAK5360.1	voltage-gated sodium channel type I	868	0
			BAC21102.1	Voltage-gated sodium channel alpha1 subunit	868	0
			BAC21101.1	voltage-gated sodium channel alpha1 subunit	868	0
			AAK00217.1	AF225985_1 voltage-gated sodium channel alpha subunit SCN1A	857	0
			AAG33412.1	voltage-gated sodium channel type II alpha subunit	803	0
			Q99250	CIN2_HUMAN Sodium channel protein, brain II alpha subunit	803	0
			AAG53413.1	voltage-gated sodium channel type II alpha subunit	803	0
			A46269	sodium channel alpha chain HBA	801	0
			NP_066287.1	sodium channel, voltage-gated, type II, alpha 2; sodium channel, voltage-gated, type II, alpha 2 polypeptide	801	0
			AAA18895.1	voltage-gated sodium channel	801	0
			Q9NY46	CIN3_HUMAN Sodium channel protein, brain III alpha subunit (Voltage-gated sodium channel subtype III)	716	0
NM_016758 NP_058038.1	Mm.1426	U:(C-HD)2.67	NP_006471.2	regulator of G-protein signalling 14; regulator of G protein signaling 14	868	0
			AAH14094.1	AAH14094 Similar to regulator of G-protein signaling 14	868	0
			O43566	RGSE HUMAN Regulator of G-protein signaling 14	827	0
			AAB92614.1	regulator of G protein signaling RGS14	545	e-158
			AAB84186.1	regulator of G protein signaling 12	353	7e-97
			AAB96644.1	regulator of G protein signaling 12	353	7e-97
			AAB84007.1	regulator of G protein signaling RGS12	350	3e-96
			NP_002917.1	regulator of G-protein signaling 12	350	3e-96
			AAC39835.1	RGS12; regulator of G-protein signaling 12	350	3e-96
			O14924	RGSC HUMAN Regulator of G-protein signaling 12 (RGS12)	350	3e-96
			AAB84114.1	regulator of G protein signalin	350	3e-96

[illegible]

	P05155	IC1_HUMAN Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh)	633	0
	ITHUC1	complement C1 inhibitor precursor [validated]	633	0
	CAA38358.1	C1 inhibitor	633	0
	CAA30314.1	C1 inhibitor	633	0
	AAM21515.1	AF435921_1 C1 esterase inhibitor	633	0
	NP_000053.1	complement component 1 inhibitor precursor, serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1	632	0
	AAB59387.1	plasma protease (C1) inhibitor precursor	632	0
	AAA35613.1	plasma protease (C1) inhibitor precursor	632	0
	CAA30469.1	C1 inhibitor (AA 135-478) (I is 2nd base in codon)	517	e-146
	AA451848.1	C1-inhibitor	454	e-127
	AA451849.1	C1 inhibitor	307	3e-83
NM_010343 NP_034473.1	Mm.1332	U ^r (C-D)2.67	367	e-101
		guathione peroxidase 5 precursor isoform 1; epididymal androgen-related protein	367	e-101
	O75715	GSHE_HUMAN Epididymal secretory glutathione peroxidase precursor(Epididymis-specific glutathione peroxidase-like protein) (BGLP)	367	e-101
	CAA06463.1	glutathione peroxidase type 5 (GPX5)	367	e-101
	CAB71121.1	dJ118GN24.2 (glutathione peroxidase 5 (epididymal androgen-related protein))	367	e-101
	P22352	GSHP_HUMAN Plasma glutathione peroxidase precursor (GSHPx-P) (Extracellular glutathione peroxidase) (GPx-P)	308	2e-83
	JQ0476	lutathione peroxidase (EC 1.1.1.19) 3, precursor [validated]	308	2e-83
	BAA00525.1	glutathione peroxidase	303	3e-82
	CAA41228.1	glutathione peroxidase	303	3e-82
	NP_002075.2	plasma glutathione peroxidase 3 precursor	295	1e-79
	AAF43005.1	extracellular glutathione peroxidase	295	1e-79
	BAA03864.1	plasma glutathione peroxidase	219	8e-57
	XP_167146.1	similar to EPIDIDYMAL SECRETORY GLUTATHIONE PEROXIDASE PRECURSOR (EPIDIDYIMIS-SPECIFIC GLUTATHIONE PEROXIDASE-LIKE PROTEIN) (EGLP)	211	2e-54

AK009460 BAB26301.1	Mm.46725	U ₁ (C-D)2.66	NP_055152.1	peptidylprolyl isomerase-like 2 isoform a; cyclophilin-like protein Cyp-60; peptidylprolyl cis-trans isomerase; cyclophilin, 60kDa	935	0
			NP_680480.1	peptidylprolyl isomerase-like 2 isoform a; cyclophilin-like protein Cyp-60; peptidylprolyl cis-trans isomerase; cyclophilin, 60kDa	935	0
			Q13356	CYP6_HUMAN Peptidyl-prolyl cis-trans isomerase like 2 (PPIase) (Cyclophilin-60) (Cyclophilin-like protein Cyp-60)	935	0
			S64705	cyclophilin-like protein Cyp-60	935	0
			AAC50376.1	cyclophilin-like protein Cyp-60	935	0
			Z207180A	cyclophilin:ISOTYPE=Cyp-60	935	0
			AAH28385.1	peptidylprolyl isomerase (cyclophilin)-like 2	934	0
			NP_680481.1	peptidylprolyl isomerase-like 2 isoform b; cyclophilin-like protein Cyp-60; peptidylprolyl cis-trans isomerase; cyclophilin, 60kDa	905	0
			AAH00022.1	AAH00022 Similar to peptidylprolyl isomerase (cyclophilin)-like 2	905	0
			AAC50378.1	cyclophilin-like protein	530 e-150	
			AAC50377.1	cyclophilin-like protein	478 e-135	
NM_023806 NP_080082.1	Mm.3311	U ₁ (C-H)2.65	NP_079105.1	hypothetical protein FLJ22662	870	0
			BAB15442.1	unnamed protein product	870	0
			AAH00909.2	AAH00909 hypothetical protein FLJ22662	397 e-110	
			NP_775813.1	hypothetical protein LOC196463	271 2e-72	
			AAH0618.1	similar to RIKEN cDNA 1300012G16	271 2e-72	
AK008273 Q61599	Mm.2241	U ₁ (C-D)2.65	NP_001166.1	Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI	270 3e-72	
			P52566	GDJS_HUMAN Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI)	270 3e-72	
			A47742	Rho-GDP-dissociation inhibitor Ly-GDI	270 3e-72	
			AAA59539.1	GDP dissociation inhibitor	270 3e-72	
			CAA49280.1	Human rho GDP-dissociation inhibitor 2 (IEF 8120)	270 3e-72	
			AAH09200.1	AAH09200 Rho GDP dissociation inhibitor (GDI) beta	270 3e-72	

AAM21075.1	AF498927	1 Rho GDP dissociation inhibitor beta	270	3c-72
ID56	B Chain B, Crystal Structure Of A Rac-RhoGdi Complex		267	2e-71
CAA45344.1	rho GDP dissociation inhibitor (GDI)		234	1e-61
NP_004300.1	Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
P32365	GDIR_HUMAN Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)		234	2e-61
I38156	rho protein GDP-dissociation inhibitor 1 (IEF 8118)		234	2e-61
IC03	E Chain E, Crystal Structure Of The RhoA-Gdp-RhoGdi Complex		234	2e-61
IC00	F Chain F, Crystal Structure Of The RhoA-Gdp-RhoGdi Complex		234	2e-61
IHH4	D Chain D, Rac1-RhoGdi Complex Involved In Naphth Oxidase Activation		234	2e-61
IHH4	E Chain E, Rac1-RhoGdi Complex Involved In Naphth Oxidase Activation		234	2e-61
BAA03096.1	human rho GDI ¹		234	2e-61
AAA3566.1	GDP dissociation inhibitor		234	2e-61
CAA49281.1	Human rho GDP-dissociation inhibitor 1(IEF 8118)		234	2e-61
AAH05851.1	AAH05851 Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
AAH05875.1	AAH05875 Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
AAH08701.1	Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
AAH09759.1	AAH09759 Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
AAH16031.1	AAH16031 Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
AAH16185.1	AAH16185 Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
AAH24258.1	Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
AAM21074.1	AF498926 1 Rho GDP dissociation inhibitor alpha		234	2e-61
AAH27730.1	Rho GDP dissociation inhibitor (GDI) alpha		234	2e-61
IFST	A Chain A, Crystal Structure Of Truncated Human RhoGdi Triple Mutant		231	1e-60
IFST	B Chain B, Crystal Structure Of Truncated Human RhoGdi Triple Mutant		231	1e-60
IFST	A Chain A, Crystal Structure Of Truncated Human RhoGdi K113a Mutant		226	6e-59
IF70	B Chain B, Crystal Structure Of Truncated Human RhoGdi K113a Mutant		226	6e-59

[illegible]

	NM_008476					A Chain A, Crystal Structure Of Truncated Rhogd K141a Mutant	IFT3	226	6e-59
	NP_032502.1	Mm.22629	U:(C-D)2.5			B Chain B, Crystal Structure Of Truncated Rhogd K141a Mutant	IFT3	226	6e-59
						A Chain A, Crystal Structure Of Rho Glt(154,155)ala Mutant	KMT	223	3e-58
						B Chain B, Crystal Structure Of Rho Glt(154,155)ala Mutant	KMT	223	3e-58
						A Chain A, Crystal Structure Of Truncated Human Rhogdt Quadruple	IFSO	223	3e-58
						A Chain A, Structure Of Rho Guanine Nucleotide Dissociation Inhibitor	IRHO	223	3e-58
						B Chain B, Structure Of Rho Guanine Nucleotide Dissociation Inhibitor	IRHO	223	3e-58
						C Chain C, Structure Of Rho Guanine Nucleotide Dissociation Inhibitor	IRHO	223	3e-58
	NN_008476					keratin 6C; keratin, epidermal type II, K6C; cytokeatrin 6C; type II keratin isoform K6c	NP_490596.1	685	0
	NP_032502.1	Mm.22629	U:(C-D)2.5			K2OC_HUMAN Keratin, type II cytoskeletal 6C (Cytokeatrin 6C) (CK 6C) (K6C keratin)	P48666	685	0
						keratin 6c, type II	i61768	685	0
						keratin type II	AAO41769.1	685	0
						keratin 6B; keratin-6B; keratin, epidermal, type II, K6B; keratin, type II cytoskeletal 6B;	NP_005546.1	681	0
						cyclokeratin 6B.	P04259	681	0
						K2CB_HUMAN Keratin, type II cytoskeletal 6B (Cytokeatrin 6B) (CK 6B) (K6B keratin)	KRHUEB	681	0
						keratin 6b, type II	AAO41768.1	681	0
						keratin type II	NP_005545.1	681	0
						keratin 6A; Keratin-6A; keratin, epidermal type II, K6A; cyclokeratin 6A; 56 cytoskeletal type II keratin	P02538	681	0
						K2CA_HUMAN Keratin, type II cytoskeletal 6A (Cytokeatrin 6A) (CK 6A) (K6A keratin)	KRHUEA	681	0
						keratin 6a, type II	AAO41767.1	681	0
						keratin type II	AAH08807.1	681	0
						AAH08807.1	AAHI4152.1	681	0
						Similar to keratin 6A	P48669	679	0
						K2CF_HUMAN Keratin, type II cytoskeletal 6F (Cytokeatrin 6F) (CK 6F) (K6F keratin)	i61771	679	0
						keratin 6f, type II			

[illegible]

		CAA68053.1	SRcyp protein	205	2e-52
NM_009542		AAH01555.1	AAH01555 Unknown (protein for MGC:5054)	205	2e-52
NP_033568.1	Mm.4417	NP_689814.1	hypothetical protein FLJ38281	548	e-155
		BAC04584.1	unnamed protein product	548	e-155
		NP_066358.1	zinc finger protein 14 (KDX 6); GIOT-4 for gonadotropin inducible transcription repressor-4	541	e-153
		P17017	ZNF14 HUMAN Zinc finger protein 14 (Zinc finger protein KOX6) (Gonadotropin inducible transcription repressor-4) (GIOT-4)	541	e-153
		BAA86990.1	gonadotropin inducible transcription repressor-4	541	e-153
		XP_032812.1	similar to hypothetical protein FLJ40981	514	e-145
		CAB66666.1	hypothetical protein	514	e-145
		NP_653290.2	hypothetical protein FLJ32191	504	e-142
		AAH26210.1	similar to unnamed protein product	504	e-142
		NP_699189.1	hypothetical protein FLJ90396	499	e-141
		BAC11261.1	unnamed protein product	499	e-141
		AAH36110.1	Similar to zinc finger protein 208	494	e-139
		AAH43151.1	Similar to zinc finger protein 208	494	e-139
		NP_057620.1	HSPC039 protein	484	e-136
		AAFP2903.1.2	AF161544 1 HSPC059	484	e-136
		NP_005806.1	zinc finger protein 443; Kruppel-type zinc finger (C2H2)	480	e-135
		BAA75543.1	Kruppel-type zinc finger protein	480	e-135
		AAH32753.1	Zinc finger protein 443	480	e-135
		JB0288	Kruppel-type zinc finger protein	477	e-134
		NP_689815.1	zinc finger protein 433	474	e-133
		BAC05279.1	unnamed protein product	474	e-133
NM_020578		NP_055415.1	EH-domain containing 3	982	0
NP_065603.1	Mm.18526	U:(C-HY)2.64	EH-domain containing 3; EH domain containing 3		

		AAF32285.1	AF214736.1 EH domain containing protein 2	982	0
		Q9NZN3	EHD3 HUMAN EH-domain containing protein 3	971	0
		AAF4047.1	AF181264.1 EH domain containing 3	971	0
		AAH33100.1	Unknown (protein for MGC:45677)	954	0
		Q9HAM9	EHD1_HUMAN EH-domain containing protein 1 (Testilin) (EPAST1)	896	0
		AAAG02009.1	similar to Homo sapiens Hpaat (HPAST) mRNA with GenBank Accession Number AF001434.1	892	0
		AAB81204.1	Hpaat	891	0
		NP_006786.1	EH-domain containing 1; homolog of Drosophila past; EH domain containing 1; testilin	877	0
		NP_644670.1	EH-domain containing 4; EH domain containing 4; ortholog of rat pincher	778	0
		Q9HZ23	EHD4 HUMAN EH-domain containing protein 4 (EH domain-containing protein FKSG7) (Hepatocellular carcinoma-associated protein 10/11)	778	0
		AAK11599.1	hepatocellular carcinoma-associated protein HCA11	778	0
		AAH06287.1	AAH06287 Unknown (protein for MGC:10356)	778	0
		AAL51079.1	AF454953.1 EH domain-containing protein-4	778	0
		AAG28784.1	AF307137.1 EH domain-containing protein FKSG7	776	0
		NP_055416.2	EH-domain containing 2; EH domain containing	744	0
		AAH14445.1	AAH14445 Unknown (protein for MGC:22994)	744	0
		AAL51078.1	AF454952.1 EH domain-containing protein-2	744	0
NM_007496		NP_008816.2	AT-binding transcription factor 1; AT motif-binding factor 1	376	6
NP_031522.1	Mm.4270	Q15911	ABF1_HUMAN Alpha-fetoprotein enhancer binding protein (AT motif-binding factor) (AT-binding transcription factor 1)	376	6
		AAC14462.1	zinc finger homeodomain protein	376	6
		2202255A	AT motif-binding factor 1	376	6
		A41948	alpha-fetoprotein enhancer-binding protein	235	6

U:(C-D)2.63

			BAA01095.1	alpha-fetoprotein enhancer binding protein	235 6
			AAC79153.1	unknown	186 5
			AAH29653.1	Unknown (protein for MGC34415)	148 1
			NP_055709.1	KIAA1056 protein	379 e-104
			Q9UPU6	Z409_HUMAN Zinc finger protein 409	379 e-104
			BAA83008.1	KIAA1056 protein	379 e-104
	U:(C-D)2.63 U:(C-H)2.57	NNM_023118 NP_075607.1	AAH03064.1	AAH03064 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)	109 8
			P98082	DAB2_HUMAN Disabled homolog 2 (Differentially expressed protein 2) (DOC-2)	109 4
			G02228	DOC-2	109 4
			AAC50824.1	DOC-2	109 4
			AAF23161.1	disabled-2	109 4
			NP_001334.1	disabled homolog 2; mitogen-responsive phosphoprotein	109 2
			AAA98975.1	DOC-2	109 2
			AAF05540.1	AF188298_1 disabled 2 p93	104 3
			AAA93195.1	differentially expressed protein	446 e-124
			AAB19032.1	mitogen-responsive phosphoprotein	366 e-100
	U:(C-D)2.62	NNM_030127 NP_084403.1	NP_444272.1	serine protease HTRA3	771 0
			P83110	HRA3_HUMAN Probable serine protease HTRA3 precursor	771 0

	AAK71475.2	serine protease HTRA3	771	0
	AAH34390.1	serine protease HTRA3	771	0
	AAH3717.1	Similar to serine protease HTRA3	771	0
	NP_002766.1	protease, serine, 11	451	e-126
	Q92743	HRA1_HUMAN Serine protease HTRA1 precursor (L56)	451	e-126
	BAA13322.1	serin protease with GGF-binding motif	451	e-126
	CAA69226.1	novel serine protease, PRSS11	451	e-126
	AAD41525.1	AF157623_1 HTRA serine protease	451	e-126
	NP_710159.1	hypothetical protein FLJ90724	383	e-106
	P83105	HRA4_HUMAN Probable serine protease HTRA4 precursor	383	e-106
	BAC11470.1	unnamed protein product	383	e-106
	AAC9721.1	serine protease	371	e-102
	NP_037379.1	protease, serine, 25 isoform 1 preproprotein; Htra-like serine protease; high temperature requirement protein A2; Omi stress-regulated endoprotease	307	5e-83
	O43464	HRA2_HUMAN Serine protease HTRA2, mitochondrial precursor (High temperature requirement protein A2) (HtraA2) (Omi stress-regulated endoprotease) (Serine proteinase OMI)	307	5e-83
	AAB94569.2	serine protease	307	5e-83
	AAF66596.1	AF141305_1 serine protease Htra2	307	5e-83
	AAH00096.1	AAH00096 Htra-like serine protease	307	5e-83
	ILCY	A Chain A, Crystal Structure Of The Mitochondrial Serine Protease Htra2	306	1e-82
	AAF66597.1	AF141306_1 serine protease Htra2-p7	258	3e-68
	AAH31082.1	protease, serine, 11 (IGF binding)	199	1e-50
	U:(C-H)/2.61	ribosomal protein S6 kinase, 70kDa, polypeptide 1; ribosomal protein S6 kinase, 70kDa, polypeptide 1; serine/threonine kinase 14 alpha	718	0
AK012045		ribosomal protein S6 kinase (EC 2.7.1.-), long splice form	718	0
BAB77991.1	Mm.34490	p70-ribosomal S6 kinase alpha-1	718	0
		KGB1_HUMAN Ribosomal protein S6 kinase (S6K) (p70-S6K)	718	0

	AAA36411.1	p70 ribosomal S6 kinase alpha-1I	718	0
	NP_002943.1	ribosomal protein S6 kinase, 70kDa, polypeptide 2; ribosomal protein S6 kinase, 70kD, polypeptide 2; p70 ribosomal S6 kinase beta	488	e-137
	BAA34402.1	p70 ribosomal S6 kinase beta	488	e-137
	Q9UBS0	K6B2_HUMAN Ribosomal protein S6 kinase beta 2 (S6K-beta 2) (70 kDa ribosomal protein S6 kinase 2) (p70-S6KB) (p70 ribosomal S6 kinase beta) (p70 S6Kbeta) (S6K2) (S6 kinase-related kinase) (SRK) (Serine/threonine-protein kinase 14 beta)	488	e-137
	AAD20990.1	S6 kinase-related kinase	488	e-137
	AAD46063.1	AF076931_1 serine/threonine kinase 14 beta	488	e-137
	AAH00094.1	AAH00094 ribosomal protein S6 kinase, 70kD, polypeptide 2	488	e-137
	AAH06106.1	AAH06106 Unknown (protein for MGC:12950)	488	e-137
	JB0377	p70 S6 kinase (EC 2.7.-.-)	485	e-136
	BAA37145.1	S6 kinase b	485	e-136
	NP_002944.2	ribosomal protein S6 kinase, 90kDa, polypeptide 1; ribosomal protein S6 kinase, 90kD, polypeptide 1; Ribosomal protein S6 kinase, 90kD, 1	272	2e-72
	Q15418	K6A1_HUMAN Ribosomal protein S6 kinase alpha 1 (S6K-alpha 1) (90 kDa ribosomal protein S6 kinase 1) (p90-RSK 1) (Ribosomal S6 kinase 1) (RSK-1) (pp90RSK1)	272	2e-72
	AAH14966.1	AAH14966 ribosomal protein S6 kinase, 90kD, polypeptide 1	272	2e-72
	AAC82495.1	ribosomal protein S6 kinase 3	272	2e-72
	NP_004577.1	ribosomal protein S6 kinase, 90kDa, polypeptide 3; ribosomal protein S6 kinase, 90kD, polypeptide 3	272	2e-72
	P51812	K6A3_HUMAN Ribosomal protein S6 kinase alpha 3 (S6K-alpha 3) (90 kDa ribosomal protein S6 kinase 3) (p90-RSK 3) (Ribosomal S6 kinase 2) (RSK-2) (pp90RSK2) (insulin-stimulated protein kinase 1) (ISPK-1)	272	2e-72
	I38556	ribosomal protein S6 kinase 2 (EC 2.7.1.-) 3	272	2e-72
	AAA81952.1	insulin-stimulated protein kinase 1	271	3e-72
	AAC82496.1	ribosomal protein S6 kinase 2	435	e-122
NM_011453		serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9		
NP_035583.1	Mm.197676	U1(C-H)2.61 (ovalbumin type)		

P50453	SPB8_HUMAN Cytoplasmic antiprotease 3 (CAP3) (CAP-3) (Protease inhibitor 9) (Serpin B9)	435 e-122
B59273	proteinase inhibitor 9	435 e-122
AAC41940.1	cytoplasmic antiprotease 3	435 e-122
AAC50793.1	erine proteinase inhibitor	435 e-122
AAH02538.1	AAH02538 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9	435 e-122
BAB91078.1	serine protease inhibitor 9	435 e-122
NP_002463.1.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)	338 7e-93
P50452	SPB8_HUMAN Cytoplasmic antiprotease 2 (CAP2) (CAP-2) (Protease inhibitor 8) (Serpin B8)	338 7e-93
A59273	proteinase inhibitor 8	338 7e-93
AAC41939.1	cytoplasmic antiprotease 2	338 7e-93
P3237	PT16_HUMAN Placental thrombin inhibitor (Cytoplasmic antiprotease) (CAP) (Protease inhibitor 6) (PI-6)	338 7e-93
AAB30320.1	cytoplasmic antiprotease; CAP	338 7e-93
AAH01394.1	AAH01394 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	338 7e-93
NP_004559.3	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)	337 2e-92
A48681	placental thrombin inhibitor	337 2e-92
CAA80373.1	thrombin inhibitor	337 2e-92
NP_109591.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil, protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived	296 4e-80
P30740	LEU_HUMAN Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI)	296 4e-80
S27383	elastase inhibitor	296 4e-80
AAC31394.1	monocyte/neutrophil elastase inhibitor	296 4e-80
AAH09015.1	AAH09015 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	296 4e-80

[illegible]

[illegible]

NM_025749			BAB21502.1	bHLH protein DEC2	223	1e-57
NP_080025.1	Mm.50930	U:(C-D)2.6	XP_068602.1	similar to RIKEN cDNA 4933409D10 [Mus musculus]	443	e-124
			BAB71507.1	unnamed protein product	414	e-115
NM_027209			NP_690591.1	membrane-spanning 4-domains, subfamily A, member 6A isoform 1; CD20-like precursor;	233	4e-61
NP_081485.1	Mm.29487	U:(C-D)2.6	NP_690591.1	membrane-spanning 4-domains, subfamily A, member 6; four-span transmembrane protein 3.2;	233	4e-61
			AAG41780.1	MS4A6A-polymorph; four-span transmembrane protein 3.1; HAIRB-iso	233	4e-61
			AAG41780.1	AF212240_1 CDA01	233	4e-61
			AAK37417.1	AF237908_1 MS4A6A protein	233	4e-61
			AAK37994.1	AF286866_1 MS4A6A-polymorph	233	4e-61
			AAH22854.1	membrane-spanning 4-domains, subfamily A, member 6A	232	7e-61
			AAAL56222.1	AF350502_1 four-span transmembrane protein 3.1	229	5e-60
			AAG44626.1	AF253977_1 HAIRB-iso	222	1e-57
				membrane-spanning 4-domains, subfamily A, member 6A isoform 2; CD20-like precursor;		
			NP_071744.2	membrane-spanning 4-domains, subfamily A, member 6; four-span transmembrane protein 3.2;	208	1e-53
			NP_071744.2	MS4A6A-polymorph; four-span transmembrane protein 3.1; HAIRB-iso	208	1e-53
			AAL07357.1	AF354930_1 MS4A6A	207	2e-53
			AAG27920.1	FI42409_1 CD20-like precursor	207	2e-53
			AAAL56223.1	AF350503_1 four-span transmembrane protein 3.2	207	3e-53
			NP_057136.1	CGH-115 protein	254	2e-67
			AAD34110.1	AF151873_1 CGH-115 protein	254	2e-67
			AAH20641.1	AAH20641 CGH-115 protein	254	2e-67
NM_008596			NP_003170.1	synaptophysin, major synaptic vesicle protein P38	219	1e-56
NP_032622.1	Mm.20942	U:(C-D)2.6	P08247	SYPH_HUMAN Synaptophysin (Major synaptic vesicle protein P38)	219	1e-56
			A35699	synaptophysin	219	1e-56
			AAAB92558.1	synaptophysin	219	1e-56

		AA05829.1	AF196779_6 synaptophysin	219	1e-56
		CAA29686.1	synaptophysin	215	3e-55
		NP_63243.1	synaptophysin	213	1e-54
		AAH22518.1	Similar to synaptophysin	213	1e-54
		CAD39117.1	hypothetical protein	213	1e-54
		AAH03681.2	AF411860_1 synaptophysin	213	1e-54
NM_023684					
NP_076173.1	Mm.28418	AAH17016.1	AAH17016 Unknown (protein for MGC:8864)	225	1e-58
		CAC03671.1	d583P15.4.1 (novel protein (translation of cDNA FLJ20406 (Em:AK000413)))	225	1e-58
		NP_060276.1	hypothetical protein FLJ20406	225	2e-58
		BAA91148.1	unnamed protein product	225	2e-58
NM_007565					
NP_031591.1	Mm.28161	AAH05010.1	AAH05010 Similar to butyrate response factor 2 (EGF-response factor 2)	416	e-116
		NP_008818.3	butyrate response factor 2; EGF-response factor 2; zinc finger protein, C3H type, 36-like 2	416	e-116
		P47974	TISD_HUMAN Butyrate response factor 2 (TIS11D protein) (EGF-response factor 2) (ERF-2)	415	e-116
		S49147	ERF-2 protein	414	e-116
		CAA5592.1	ERF-2	414	e-116
		AAA91778.1	Tis11d	414	e-116
NM_008986					
NP_033012.1	Mm.8009	NP_036364.1	polymerase I and transcript release factor; RNA polymerase I and transcript release factor, TTF-1 interacting peptide 12	616	e-176
		AA027093.1	AF312393_1 leucine-zipper protein FKSG13	616	e-176
		AAC63404.1	TTF-1 interacting peptide 12	330	3e-90
		AAH04295.1	AAH04295 Unknown (protein for IMAGE3622356)	323	3e-88
		AAH08849.1	AAH08849 Unknown (protein for MGC:14316)	315	1e-85
NM_033398					
NP_203971.1	Mm.24997	AAH47003.1	PTDSR protein	765	0
		BAA25511.1	KJAA0585 protein	764	0

			NP_055982.1	phosphatidylserine receptor; phosphatidylserine receptor beta	702
			BAAC16755.1	phosphatidylserine receptor beta	702
NM_008103					
NP_032129.1	Mm.1400	U:(C-HI)2.56	BAA77250.2	GCM motif protein	674
			BAA94757.1	chorion-specific transcription factor GCMa	674
			BAB18039.1	chorion-specific transcription factor GCMa	674
			NP_003634.1	glial cells missing homolog a; glial cells missing homolog 1	669
			BAA13651.1	hGCMa	669
			NP_004743.1	glial cells missing homolog 2; glial cells missing homolog b (Drosophila)	250
			AAC33792.1	glial cells missing protein homolog	250
			AAC98097.1	glide/gcm protein homolog	250
			BAA94758.1	chorion-specific transcription factor GCMa	216
					457
NM_009914			NP_001828.1	chemokine (C-C motif) receptor 3	e-128
NP_034044.1	Mm.57050	U:(C-D)2.55		CCR3 HUMAN C-C chemokine receptor type 3 (C-C CCR-3) (CCR-3)	457
			P51677	(CCR3)(CCR3) (Eosinophil eotaxin receptor)	e-128
			AAC50469.1	CC chemokine receptor 3	457
			AAB16831.1	eosinophil eotaxin receptor	e-128
			AAB82589.1	chemokine receptor	457
			AAL85154.1	AF247361_1 CC chemokine receptor 3	e-128
			AAH35141.1	similar to chemokine (C-C motif) receptor 3	457
			G02436	chemokine (C-C) receptor 3	e-128
			AAB09726.1	C-C chemokine receptor 3	456
			BAA86964.1	b-chemokine receptor CCR3	e-128
			NP_001286.1	chemokine (C-C motif) receptor 1; RANTES receptor	452
				CCR1_HUMAN C-C chemokine receptor type 1 (C-C CCR-1) (CCR-1) (CCR1)	e-118
			P32246	(Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R) (RANTES-R) (HM145) (LD78 receptor)	422

			A45177	chemokine (C-C) receptor 1	422	e-118
			AAA38408.1	C-C chemokine receptor type 1	422	e-118
			AAA36549.1	macrophage inflammatory protein-1-alpha	422	e-118
			BAA01725.1	HM145	421	e-118
			AAB65715.1	CCR5 receptor	357	1e-98
			AAB65712.1	CCR5 receptor	357	1e-98
			AAB65730.1	CCR5 receptor	357	2e-98
			AAB65725.1	CCR5 receptor	357	2e-98
			AAB65701.1	CCR5 receptor	357	2e-98
NM_030714					550	e-156
NP_109639.1	Mm.29197	U:(C-D)2.55	BAC03801.1	unnamed protein product	540	e-152
			BAC04344.1	unnamed protein product	237	5e-62
			CAD38593.1	hypothetical protein	215	2e-55
			NP_612144.1	rhysin 2	215	2e-55
			AAL90859.1	AF484416_1 rhysin 2	215	2e-55
			AAH42191.1	similar to rhysin 2,	215	2e-55
AK020110					199	2e-51
BAB31998.1	Mm.180813	U:(C-D)2.55	NP_112177.1	hypothetical protein DKFZp5661091	199	2e-51
			CAB66638.1	hypothetical protein	233	6e-62
NM_013590					233	6e-62
NP_038618.1	Mm.177539	U:(C-D)2.55	NP_000230.1	lysozyme precursor	233	6e-62
			P00695	LYC HUMAN Lysozyme C precursor (1,4-beta-N-acetylmuramidase C)	233	6e-62
			LZHU	lysozyme (EC 3.2.1.17) c precursor [validated]	233	6e-62
			AAA59335.1	lysozyme precursor (EC 3.2.1.17)	233	6e-62
			AAA59336.1	lysozyme precursor (EC 3.2.1.17)	233	6e-62
			AAH04147.1	AAH04147 lysozyme (renal amyloidosis)	233	6e-62
			AAA36188.1	lysozyme precursor (EC 3.2.1.17)	233	9e-62

[illegible]

		NP_005060.1	single-minded (Drosophila) homolog 2 long isoform; human transcription factor SIM2, homolog of the Drosophila single-minded gene SIM1	233	5e-61
		Q14190	SIM2 HUMAN Single-minded homolog 2	233	5e-61
		AAB02396.1	transcription factor SIM2 long form	233	5e-61
		BAA89433.1	single-minded 2 protein	233	5e-61
NM_019408	Mm20225 U:(C-D)2.54	Q00653	KBP2 HUMAN Nuclear factor NF-kappa-B p100/p49 subunits (H2TF1) (Oncogene Lys10) (Lys10) [Contains: Nuclear factor NF-kappa-B p52 subunit]	140	3
NP_062281.1		AAH02844.1	AAH02844 Similar to nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100 [Homo sapiens]	140	3
		CAC08399.1	ba18114.2.1 (nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) isoform 1)	139	9
		A42024	transcription factor NF-kappa-B2, p100 splice form	138	9
		AAB21124.1	p50-NF-kappa B homolog	138	9
		AAB23437.1	p98-Re(NF-kappa B p105 homolog [human, T lymphocytes, Peptide, 900 aa]	138	3
		NP_002493.2	nuclear factor of kappa light polypeptide gene enhancer in B-cells2 (p49/p100); Nuclear factor of kappa light chain gene enhancer in B-cells 2	137	0
		S17233	transcription factor NF-kappa-B2, p105 splice form	137	0
		CAA43715.1	NF-kB subunit	137	0
		I38609	transcription factor NF-kappa-B2, p80 splice form	104	3
		AAA21462.1	p80HT	104	3
		CAC08398.1	ba18114.2.2 (nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) isoform 2)	689	0
		A57034	transcription factor NF-kappa-B2, p49 splice form	687	0

		CAA43716.1	NF-kB subunit	687	0
		IA3Q	A Chain A, Human NF-Kappa-B P52 Bound To Dna	567	e-161
		IA3Q	B Chain B, Human NF-Kappa-B P52 Bound To Dna	567	e-161
X80339		NP_005973.1	sine oculis homeobox (Drosophila) homolog 1	495	e-140
CAA56585.1	Mm.4645	Q15475	SIX1_HUMAN Homeobox protein SIX1 (Sine oculis homeobox homolog 1)	495	e-140
		CAA62974.1	six1	495	e-140
		AAK06772.1	AF323497_1 SIX1	495	e-140
		AAH08874.1	AAH08874 sine oculis homeobox (Drosophila) homolog 1	492	e-139
		AAK16381.1	AF332196_1 SIX2	374	e-103
		Q9NPC8	SIX2_HUMAN Homeobox protein SIX2 (Sine oculis homeobox homolog 2)	374	e-103
		AAF69031.1	AF136939_1 sine oculis homeobox homolog 2	374	e-103
		AAF69032.1	AF136940_1 sine oculis homeobox homolog 2	374	e-103
		AAK06773.1	AF323498_1 SIX2	374	e-103
		AAK16582.1	AF332197_1 SIX2	374	e-103
		AAK16583.1	AF332198_1 SIX2	374	e-103
		NP_053628.2	sine oculis homeobox homolog 2	372	e-103
		AAH24033.1	sine oculis homeobox homolog 2 (Drosophila)	372	e-103
		NP_031400.1	sine oculis homeobox homolog 6; optic homeobox 2; sine oculis homeobox (Drosophila) homolog 6; sine oculis homeobox homolog 6 (Drosophila)	268	2e-71
		Q95475	SIX6_HUMAN Homeobox protein SIX6 (Sine oculis homeobox homolog 6) (Optic homeobox 2) (Homeodomain protein OPTX2)	268	2e-71
		CAA09773.1	Six9 protein	268	2e-71
		AAD49844.1	AF141651_1 homeobox containing transcription factor SIX6	268	2e-71
		AAF04402.1	AF031648_1 homeodomain protein OPTX2	268	2e-71
		NP_005404.1	sine oculis homeobox homolog 3	265	2e-70
		Q95343	SIX3_HUMAN Homeobox protein SIX3 (Sine oculis homeobox homolog 3)	265	2e-70

	AAAD11939.1	homeobox protein Six3	265	2e-70
	AAAD15753.1	Six3	265	2e-70
	CAB42539.1	SIX3 protein	265	2e-70
	AAAD51091.1	SIX3 protein	265	2e-70
	NP_059116.1	sine oculis homeobox homolog 4	260	7e-69
	Q9JUI6	SIX4_HUMAN Homeobox protein SIX4 (Sine oculis homeobox homolog 4)	260	7e-69
	BAA86223.1	SIX4	260	7e-69
	AAAF04403.1	AF032107.1 AREC3	234	5e-61
	BAA94484.1	homeodomain protein OPTX2	225	2e-58
	NP_000046.1	butyrylcholinesterase precursor	100	8
	P06276	CHLE_HUMAN Cholinesterase precursor (Acetylcholine acylhydrolase) (Choline esterase II) (Butyrylcholine esterase) (Pseudocholinesterase)	100	8
	ACHU	cholinesterase (EC 3.1.1.8) precursor [validated]	100	8
	AAA98113.1	cholinesterase (EC 3.1.1.8)	100	8
	AAA52015.1	butyrylcholinesterase (EC 3.1.1.8)	100	8
	AAA99296.1	butyrylcholinesterase	100	8
	AAH18141.1	AAH18141 butyrylcholinesterase	100	8
	NP_000656.1	acetylcholinesterase lyticophilic form precursor	638	0
	P22303	ACES_HUMAN Acetylcholinesterase precursor (ACHE)	638	0
	A39256	acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form	638	0
	AAA68151.1	acetylcholinesterase	638	0
	1FRU	A Chain A, Crystal Structure Of Mutant E202q Of Human Acetylcholinesterase Complexed With Green Mamba Venom Peptide Fasciculin-II	636	0
NM_009738				
NP_033868.1	Mm.8073	U1(C-D)2.53		

		NP_056646.1	acetylcholinesterase PI-linked form precursor	588	e-167	
		IB41	A Chain A, Human Acetylcholinesterase Complexed With Fasciculin-II, Glycosylated Protein	587	e-167	
		AAO32948.1	AF334270.1 apoptosis-related acetylcholinesterase	365	e-101	
		NP_065793.1	neuroigin 4; neuroigin X	308	2e-83	
		AAM46112.1	AF376803.1 neuroigin X	308	2e-83	
		AAH34018.1	NLGN4 protein	308	2e-83	
		BAA86574.1	KIAA1260 protein	308	2e-83	
		AAM46113.1	AF376804.1 neuroigin Y	306	5e-83	
		XP_113932.3	similar to neuroigin 2 [Rattus norvegicus]	303	4e-82	
		AAM46111.1	AF376802.1 neuroigin 2	303	4e-82	
NM_011792				925	0	
NP_035922.2	Mm.24044	U:(C-D)2.53	KIAA1149 protein			
			beta-site APP-cleaving enzyme 1 isoform A preproprotein; beta-site amyloid beta A4 precursor protein-cleaving enzyme; APP beta-secretase; aspartyl protease 2; beta-site amyloid precursor protein cleaving enzyme; memapsin-2; membrane-associated aspartic protease 2; transmembrane aspartic proteinase Asp2; beta-secretase	954	0	
			BACE HUMAN Beta-secretase precursor (Beta-site APP cleaving enzyme) (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2) (Memapsin-2)	954	0	
			P56817	954	0	
			A59090	954	0	
			aspartic proteinase (EC 3.4.23.-) BACE precursor	954	0	
			AAF04142.1	AF190725.1 beta-site APP cleaving enzyme	954	0
			AAE17079.1	aspartyl protease 2	954	0
			AAF18982.1	AF201468.1 APP beta-secretase	954	0
			AAF26367.1	AF204943.1 transmembrane aspartic proteinase Asp 2	954	0
			AAH36084.1	beta-site APP-cleaving enzyme	952	0
			AAF13715.1	AF200193.1 memapsin 2	953	0

		beta-site APP-cleaving enzyme 1 isoform B preproprotein; beta-site amyloid beta A4 precursor protein-cleaving enzyme; APP beta-secretase; aspartyl protease 2; beta-site amyloid precursor protein cleaving enzyme; memapsin-2; membrane-associated aspartic protease 2; transmembrane aspartic proteinase Asp2; beta-secretase	890	0
NP_020428.1		beta-site APP cleaving enzyme L476	890	0
BAB40931.1		AF338816_1 beta-site APP cleaving enzyme type B	890	0
AAK38374.1		beta-site APP-cleaving enzyme 1 isoform C preproprotein; beta-site amyloid beta A4 precursor protein-cleaving enzyme; APP beta-secretase; aspartyl protease 2; beta-site amyloid precursor protein cleaving enzyme; memapsin-2; membrane-associated aspartic protease 2; transmembrane aspartic proteinase Asp2; beta-secretase	846	0
NP_020427.1		beta-site APP cleaving enzyme L457	846	0
BAB40932.1		AF338817_1 beta-site APP cleaving enzyme type C	846	0
AAK38375.1		A Chain A, Structure Of Beta-Secretase Complexed With Inhibitor	795	0
IFKN		B Chain B, Structure Of Beta-Secretase Complexed With Inhibitor	795	0
IFKN		A Chain A, Crystal Structure Of Beta-Secretase Complexed With Inhibitor Orm00-3	795	0
IM4H		B Chain B, Crystal Structure Of Beta-Secretase Complexed With Inhibitor Orm00-3	795	0
IM4H		beta-site APP-cleaving enzyme 1 isoform D preproprotein; beta-site amyloid beta A4 precursor protein-cleaving enzyme; APP beta-secretase; aspartyl protease 2; beta-site amyloid precursor protein cleaving enzyme; memapsin-2; membrane-associated aspartic protease 2; transmembrane aspartic proteinase Asp2; beta-secretase	585	e-166
NP_020429.1		beta-site APP cleaving enzyme L432	585	e-166
BAB40933.1		beta-site APP-cleaving enzyme 2 isoform A preproprotein; beta secretase 2; aspartyl protease 1; membrane-associate aspartic protease 1; memapsin-1; Down syndrome region aspartic protease; 56 kDa aspartic-like protease; beta-site amyloid beta A4 precursor protein-cleaving enzyme 2; transmembrane aspartic proteinase Asp1	452	e-126
NP_030237.2		BAF2_HUMAN Beta secretase 2 precursor (Beta-site APP-cleaving enzyme 2) (Aspartyl protease 1) (Asp 1) (ASPI) (Membrane-associated aspartic protease 1) (Memapsin-1)	452	e-126
Q9Y5Z0		aspartic-like protease	452	e-126
AAD45240.1		AF050171_1 aspartyl protease	452	e-126
AAD45963.1		aspartyl protease 1	452	e-126
AAFI7078.1			452	e-126

			AAF26368.1	AF204944.1	transmembrane aspartic proteinase Asp 1	452	e-126
			AAF29494.1	AF178532.1	aspartyl protease	452	e-126
			AAH14453.1	AAH14453	Unknown (protein for MGC:23029)	452	e-126
			AAF13714.1	AF200192.1	memapsin 1	452	e-126
NM_011603					TBP-like 1; TBP-like protein; TBP-related factor 2; TATA box binding protein-related factor 2;		
NP_035733.1	Mm28415	U:(C-D)2.53	NP_004856.1	21-kDa TBP-like protein; second TBP of unique DNA		369	e-102
			O95753	TLP1_HUMAN TATA box binding protein-like protein 1 (TBP-like protein 1) (TATA box binding protein-related factor 2) (TBP-related factor 2) (STUD protein) (21-kDa TBP-like protein)		369	e-102
			JG0162	TBP-like protein		369	e-102
			BAA75218.1	TBP-like protein		369	e-102
			AAD24800.1	AF130312.1	STUD protein	369	e-102
			AAD28785.1	AF136570.1	TATA box binding protein-related factor 2	369	e-102
			AAH17559.1	AAH17559	TBP-like 1	369	e-102
			AAH00381.1	AAH00381	TBP-like 1	367	e-101
NM_009748							
NP_033878.1	Mm23564	U:(C-D)2.52	NP_005859.1	BET1 homolog; Golgi vesicular membrane trafficking protein p18; Bet1p homolog		194	3e-50
			O15155	BET1_HUMAN BET1 homolog (Golgi vesicular membrane trafficking protein p18) (HBET1)		194	3e-50
			AAB62941.1	Bet1p homolog		194	3e-50
			AAD47132.1	AC006378.1	Bet1p homolog	194	3e-50
			AAH00899.1	AAH00899	Golgi vesicular membrane trafficking protein p18	194	3e-50
					CD40 antigen ligand; CD40 antigen ligand (hyper-IgM syndrome); T-B cell-activating molecule; TNF-related activation protein	194	3e-50
NM_011616			NP_000065.1				
NP_035746.2	Mm4861	U:(C-D)2.52				401	e-111
					TNF5_HUMAN Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (TNF-related activation protein) (TRAP) (T cell antigen Gp39) (CD154 antigen)	401	e-111
					CD40 ligand	401	e-111
			CAA48554.1	CD40 ligand		401	e-111
			CAA48077.1	CD40 ligand		401	e-111

		CAA78737.1	glycoprotein 39	401	e-111
		AAA35662.1	CD40 surface protein	401	e-111
		BAA06599.1	CD40 ligand	401	e-111
		AAB25206.1	gp39=CD40 ligand [human, hyper-IgM syndrome patient JW, T cells, Peptide Partial Mutant, 151 aa]	226	7e-59
		AAB25207.1	gp39=CD40 ligand [human, hyper-IgM syndrome patient CD, T cells, Peptide Partial Mutant, 151 aa]	223	4e-58
		I19Y	Crystal Structure Of Human CD40 Ligand	221	2e-57
		I19R	A Chain A, Structure Of Cd40l In Complex With The Fab Fragment Of Humanized 5c8 Antibody	221	2e-57
		I19R	B Chain B, Structure Of Cd40l In Complex With The Fab Fragment Of Humanized 5c8 Antibody	221	2e-57
		I19R	C Chain C, Structure Of Cd40l In Complex With The Fab Fragment Of Humanized 5c8 Antibody	221	2e-57
NM_008715			DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26; RNA helicase HDB; deleted in cancer 1;	141	
NP_032741	Mm_4173	NP_036273.1	RNA helicase HDB/DICE1; DEAD box protein	6	0
		AAF03046.1	candidate tumor suppressor protein DICE1	141	0
		AAH39829.1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	141	0
		AAD39481.1	AF141326, 1 RNA helicase HDB/DICE1	116	0
		T17730	hypothetical protein DKFZp434B105.1	879	0
		CAB5620.1	hypothetical protein	879	0
		NP_077719.2	notch 2 preproprotein	581	e-165
		Q04721	NTC2, HUMAN Neurogenic locus notch homolog protein 2 precursor (Notch 2) (nN2)	581	e-165
		AAA36377.2	NOTCH 2	581	e-165
		AAG37073.1	AF315356, 1 NOTCH2 protein	577	e-164
		AAH10154.1	AAH10154 Unknown (protein for IMAGE:3623163)	492	e-138
		BAC11381.1	unnamed protein product	475	e-133

U:(C-HI)2.51

			XP_209691.1	similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26; deleted in cancer 1; RNA helicase HDB/DICE1; DEAD box protein; RNA helicase HDB	456 e-132
			AAH19835.1	AAH19835 Notch homolog 2 (Drosophila)	449 e-125
NM_011086			XP_028867.2	similar to FYVE finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate 5-kinase) (PIP5K) (PtdIns(4)P-5-kinase) (p235)	186 e-125
			BAC03674.1	unnamed protein product	186 e-125
			Q9Y217	FYV1_HUMAN FYVE finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate 5-kinase) (PIP5K) (PtdIns(4)P-5-kinase) (p235)	107 e-125
			BAA76825.1	KIAA0981 protein	107 e-125
			NP_639884.1	hypothetical protein MGC40423	572 e-162
			AAH32389.1	similar to FYVE finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) (p235)	572 e-162
NM_013820			NP_000180.2	hexokinase 2; hexokinase-2, muscle	173 e-162
NP_038848.1	Mm.2549	U:(C-D)1.77	AAH20174.1	AF148513.1 hexokinase II	173 e-162
			AAH21116.1	AAH21116 hexokinase 2	173 e-162
			P52789	HYK2_HUMAN Hexokinase, type II (HK II) (Muscle form hexokinase)	173 e-162
			JC2025	hexokinase (EC 2.7.1.1) II	173 e-162
			CAA8651.1	Human hexokinase II cDNA	173 e-162
			CAA86476.2	hexokinase II	172 e-162
			HKHB	A Chain A, Crystal Structure Of Recombinant Human Brain Hexokinase Type I Complexed With Glucose And Glucose-6-Phosphate	138 e-162

	1HKB	B Chain B, Crystal Structure Of Recombinant Human Brain Hexokinase Type I Complexed With Glucose And Glucose-6-Phosphate	138	9	0
	AAC15862.1	AAC15862 hexokinase I	138	9	0
	AAH08730.1	AAH08730 hexokinase 1	138	9	0
	1HKC	A Chain A, Recombinant Human Hexokinase Type I Complexed With Glucose And Phosphate	138	7	0
	1QHA	A Chain A, Human Hexokinase Type I Complexed With Atp Analogue Amp-Pnp	138	7	0
	1QHA	B Chain B, Human Hexokinase Type I Complexed With Atp Analogue Amp-Pnp	138	7	0
	NP_000179.1	hexokinase 1 isoform HK1; brain form hexokinase	138	6	0
	P19367	HXYK1_HUMAN Hexokinase, type I (HK I) (Brain form hexokinase)	138	6	0
	A31869	hexokinase (BC 2.7.1.1) I [validated]	138	6	0
	AAAS2646.1	hexokinase 1	138	6	0
	1CZA	N Chain N, Mutant Monomer Of Recombinant Human Hexokinase Type I Complexed With Glucose, Glucose-6-Phosphate, And Atp	138	3	0
	1DQK	N Chain N, Mutant Monomer Of Recombinant Human Hexokinase Type I With Glucose And Atp In The Active Site	138	1	0
	NP_277032.1	hexokinase 1 isoform HK1-a/b; brain form hexokinase	136	8	0
	NP_277033.1	hexokinase 1 isoform HK1-a/b; brain form hexokinase	136	8	0
	AAF82319.1	AAF82319 hexokinase 1 isoform ta/b	136	8	0

				NP_277035.1	hexokinase 1 isoform HK1-td; brain form hexokinase	136 8	0
				AAF82320.1	AAF82320 hexokinase 1 isoform td	136 8	0
NM_007381 NP_031407.1	Mm.2445	U:(C-D)1.74		P_001599.1	acyl-Coenzyme A dehydrogenase, long chain precursor	727	0
				AA0559	long-chain-acyl-CoA dehydrogenase (EC 1.3.99.13) precursor, mitochondrial	727	0
				AAAS1565.1	long chain acyl-CoA dehydrogenase	727	0
				AAH39063.1	Similar to acyl-Coenzyme A dehydrogenase, long chain	727	0
				1911479A	A long chain acyl-CoA dehydrogenase	727	0
				P28330	ACDL HUMAN Acyl-CoA dehydrogenase, long-chain specific, mitochondrial precursor (LCAD)	725	0
				AAH17202.1	AAH17202 isovaleryl Coenzyme A dehydrogenase	234	2e-61
				NP_002216.1	isovaleryl Coenzyme A dehydrogenase	234	2e-61
				P26440	IVD HUMAN isovaleryl-CoA dehydrogenase, mitochondrial precursor (IVD)	234	2e-61
				A37033	isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor	234	2e-61
				AAAS2711.1	isovaleryl-coA dehydrogenase (IVD)	234	2e-61
				AAF20182.1	isovaleryl dehydrogenase	234	2e-61
				1IVH	A Chain A, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	234	2e-61
				1IVH	B Chain B, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	234	2e-61
				1IVH	C Chain C, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	234	2e-61
				1IVH	D Chain D, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	234	2e-61
				NP_000008.1	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain precursor	217	4e-56
				P16219	ACDS HUMAN Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor (SCAD) (Bueryl-CoA dehydrogenase)	217	4e-56

		A30605	acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, short-chain-specific	217	4e-56
		AAA60307.1	short chain acyl-CoA dehydrogenase precursor (EC 1.3.99.2)	217	4e-56
		CAB02492.1	acyl-CoA dehydrogenase	217	4e-56
		AAD00552.1	short chain acyl CoA dehydrogenase	217	4e-56
		1704375A	short chain acyl-CoA dehydrogenase	217	4e-56
		AAH25963.1	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	214	2e-55
		CAD38535.1	hypothetical protein	209	6e-54
		NP_001600.1	acyl-Coenzyme A dehydrogenase, short/branched chain precursor	209	7e-54
		P45954	ACDB HUMAN Acyl-CoA dehydrogenase, short/branched chain specific, mitochondrial precursor (SBCAD) (2-methyl branched chain acyl-CoA dehydrogenase) (2-MEBCAD) (2-methylbutyryl-coenzyme A dehydrogenase) (2-methylbutyryl-CoA dehydrogenase)	209	7e-54
		A55680	acyl-CoA dehydrogenase (EC 1.3.99.3) short/branched chain specific precursor	209	7e-54
		AAA74424.1	acyl-CoA dehydrogenase	209	7e-54
		AAF97921.1	short/branched chain acyl-CoA dehydrogenase	209	7e-54
		AAH13756.1	AAH13756 Unknown (protein for MGC:21286)	209	7e-54
NM_026268		AAH05047.1	AAH05047 Unknown (protein for MGC:12852)	652	0
NP_080544.1	Mm.1791	U3(C-D)1.66	dual specificity phosphatase 6	652	0
		AAH37236.1	dual specificity phosphatase 6 isoform a; MAP kinase phosphatase 3; serine/threonine specific protein phosphatase	651	0
		NP_001937.1	DUS6_HUMAN Dual specificity protein phosphatase 6 (Mitogen-activated protein kinase phosphatase 3) (MAP kinase phosphatase 3) (MKP-3) (Dual specificity protein phosphatase PYST1)	651	0
		Q16828	protein-tyrosine-phosphatase	651	0
		CAA63813.1	DUSP6	651	0
		BAA31968.1	DUSP6	651	0
		BAA34369.1	DUSP6	651	0
		AAH03562.1	AAH03562 dual specificity phosphatase 6	651	0
		AAH03143.1	AAH03143 dual specificity phosphatase 6	651	0

				XP_037430.6	similar to dual-specificity phosphatase 7 PYS12-L	473	e-133
				AAAM77606.1	AF508727_1 dual-specificity phosphatase 7 PYS12-L	473	e-133
				CAA63814.1	protein-tyrosine-phosphatase	415	e-115
				Q16829	DUS7_HUMAN Dual specificity protein phosphatase 7 (Dual specificity protein phosphatase PYS12)	412	e-114
				AAH19107.1	AAH19107 Unknown (protein for MGC:29817)	412	e-114
				NP_001386.1	dual specificity phosphatase 9; map kinase phosphatase 4; serine/threonine specific protein phosphatase	314	4e-85
				Q99956	DUS9_HUMAN Dual specificity protein phosphatase 9 (Mitogen activated protein kinase phosphatase 4) (MAP kinase phosphatase 4) (MKP-4)	314	4e-85
				CAA69610.1	mitogen-activated protein kinase phosphatase 4	314	4e-85
				IMKP	Crystal Structure Of An Active Site Mutant Of The Pyst1	288	4e-77
				IHZM	A Chain A. Structure Of Erk2 Binding Domain Of Mapk Phosphatase Mkp-3: Structural Insights Into Mkp-3 Activation By Erk	274	5e-73
				AAH34936.1	Similar to dual specificity phosphatase 9	266	9e-71
				AAH42166.1	Similar to dual specificity phosphatase 9	266	9e-71
				NP_006396.2	transmembrane 9 superfamily member 1; multispanning membrane protein (70kD); transmembrane protein 9 superfamily member 1	109	1 0
NM_028780						109	1 0
NP_083056.2				AAH10856.1	AAH10856 Unknown (protein for MGC:9160)	109	1 0
				CAD61879.1	unnamed protein product	108	1 0
				O15321	TS91_HUMAN Transmembrane 9 superfamily protein member 1 precursor (bMP70)	108	1 0
				AAC51782.1	multispanning membrane protein	108	1 0
				CAD61941.1	unnamed protein product	830	0
				Q9HDA5	TS93_HUMAN Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-iso)	313	7e-85

			AAF21983.1	SNM-11044 binding protein	313	7e-85
			AAF98159.1	AF269150_1 transmembrane protein TM9SF3	313	9e-85
			BAB55569.1	unnamed protein product	306	1e-82
			NP_055557.1	KIAA0255 gene product	292	2e-78
			Q92544	T9S4_HUMAN Transmembrane 9 superfamily protein member 4	292	2e-78
			BAA13385.1	Similar to Scerevisiae EMP70 protein precursor (S25110)	292	2e-78
			CAB75607.2	d183GN17.2 (KIAA0255 protein)	292	2e-78
			AAH21107.1	AAH21107 KIAA0255 gene product	292	2e-78
			AAH22850.1	KIAA0255 gene product	292	2e-78
			NP_064508.1	endomembrane protein emp70 precursor isolog	265	2e-70
			AAF67014.1	AF160213_1 endomembrane protein emp70 precursor isolog	265	2e-70
			NP_004791.1	transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2	265	2e-70
			Q99805	T9S2_HUMAN Transmembrane 9 superfamily protein member 2 precursor (p76)	265	2e-70
			AAB38973.1	p76	265	2e-70
NM_007912			P00533	PCFR_HUMAN Epidermal growth factor receptor precursor (Receptor protein-tyrosine kinase ErbB-1)	116	0
NP_031938.1	Mm.8534	U:(C-HD)1.67			0	0
			AAG35789.1	AF288738_4 p170 epidermal growth factor receptor	116	0
			AA522711.1	aberrant epidermal growth factor receptor	116	0
			AAG35788.1	AF288738_3 A431-specific p115 epidermal growth factor receptor	116	0
			GOHUE	epidermal growth factor receptor precursor	115	0
			CAA25240.1	epidermal growth factor receptor	115	0
			1006266A	epidermal growth factor receptor	115	0

			IIVO	A Chain A, Crystal Structure Of The Complex Of Human Epidermal Growth Factor And Receptor Extracellular Domains.	115	7
			IIVO	B Chain B, Crystal Structure Of The Complex Of Human Epidermal Growth Factor And Receptor Extracellular Domains.	115	7
			AAG35786.1	AF288738_1 p110 epidermal growth factor receptor	114	1
			AAG43240.1	AF125253_1 truncated epidermal growth factor receptor precursor	114	1
			AAG35790.1	AF288738_5 truncated epidermal growth factor receptor	114	1
			AAG35790.1	AF288738_5 truncated epidermal growth factor receptor	114	1
			CAA25282.1	EGF (1 is 2nd base in codon)	942	0
			1007208A	epidermal growth factor receptor	884	0
			AAC50802.1	epidermal growth factor receptor precursor	700	0
			AAB53063.1	truncated epidermal growth factor receptor-like protein precursor	700	0
			AAG35787.1	AF288738_2 p60 epidermal growth factor receptor	700	0
			NP_005226.1	v-erb-a erythroblastic leukemia viral oncogene homolog 4; avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 4; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4	626	e-179
			Q15303	HERB4_HUMAN Receptor protein-tyrosine kinase erbB-4 precursor (p180-erbB4) (Tyrosine kinase-type cell surface receptor HER4)	626	e-179
			A47253	epidermal growth factor receptor, HER4	626	e-179
			AAB59446.1	receptor tyrosine kinase	626	e-179
			NP_005671.1	TBP-associated factor 1B: TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, G3RD; SL1, G3KD subun	836	0
			AAH18137.1	AAH18137 Unknown (protein for MGC-9349)	835	0
			I61581	transcription factor SL1	738	0
			AAAG2863.1	transcription factor SL1	738	0
			U:(C-HD)1.56			
			MM39082			
			NP_005639.1			
			MM_020614			

AK016618 BAB30341.1	Mm.40169	U:(C-D)+2.0 U:(C-IR)+1.9	NP_078808	PF20; sperm-associated WD repeat protein	548	1e-156
AK016718 XP_111038	Mm.23534	U:(C-D)+2.2 U:(C-IR)+1.9	BAB71464	unnamed protein product	431	0
			NP_114104	teklin 3; testicular microtubules-related protein	431	0
			AAH31688	TEK13 protein	429	0
			NP_653275	hypothetical protein FLJ32871	288	1e-110
			NP_444515	teklin 1	168	2e-59
NN_008919 2207219A	Mm.57059	U:(C-D)+1.9 U:(C-IR)+1.9	NP_005963	pancreatic polypeptide receptor 1	563	1e-159
			G02300	pancreatic polypeptide receptor	562	1e-158
			AAA59920	neuropeptide y receptor	318	6e-85
			NP_000900	neuropeptide Y receptor Y1; Neuropeptide Y receptor	316	2e-84
NN_018789 Q9WYH3	Mm.88827	U:(C-D)+1.8 U:(C-IR)+1.8	P98177	Putative fork head domain transcription factor AFX1 (Forkhead box protein O4).	824	0
			NP_005929	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7;	809	0
				myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 7		
			CAA72156	AFX1	798	0
			AAI85197	forkhead transcription factor AFX variant zeta	678	0
			NP_001446	forkhead box O3A; forkhead (Drosophila) homolog (rhabdomyosarcoma) like 1; forkhead, Drosophila, homolog of, in rhabdomyosarcoma-like 1	319	1e-85
			NP_002006	forkhead box O1A; forkhead (Drosophila) homolog 1 (rhabdomyosarcoma); forkhead, Drosophila, homolog of, in rhabdomyosarcoma	298	2e-79
			Q12778	Forkhead box protein O1A (Forkhead in rhabdomyosarcoma).	298	2e-79

			1E17_A	Chain A, Solution Structure Of The Dna Binding Domain Of The Human Forkhead Transcription Factor Afx (Foxo4).	227	5e-58
			CAA04860	fork head protein	205	2e-51
NM_021371	Mm.100980	U:(C-D)+2.3	NP_113656	calneuron 1; calcium-binding protein CABP8	412	1e-114
NP_067346.1		U:(C-IR)+1.9				

Subtable 1C: Mixed Mouse Genes/Proteins and the Corresponding Human Proteins

Accession Number	Gene Name	Protein Name	Accession Number	Protein Name	Accession Number	Protein Name
NM_009020	U1(C-D)2.52	U1(C-D)2.52	P55895	RAG2 HUMAN V(D)J recombination activating protein 2 (RAG-2)	1003	0
NP_033046.1	F1(R-D)+4.59	F1(R-D)+4.59	NP_000527.1	recombination activating gene 2	999	0
			AAG38705.1	recombination activating protein 2	289	9,00e-78
			AAC35287.1	RAG2	211	2.00e-54

Master Table 2: Human Protein Classes
Subtable 2A: Classes Corresponding to Favorable Mouse Genes/Proteins

Gene/Protein	Score	Class
AK013950 NP_079929.1	F:(C-D)+8.51 F:(C-IR)+3.76	HSPC232
NM_013459 NP_038487.1	F:(C-D)+3.03 F:(IR-D)+7.17	complement factor
		complement factor D
		Complement factor D precursor (C3 convertase activator) (Properdin factor D) (Adipsin)
NM_009104 NP_033130.1	F:(C-D)+7.08	ribonucleotide reductase
		small subunit ribonucleotide reductase
		ribonucleotide reductase M2 subunit; ribonucleotide reductase M2 polypeptide
		Ribonucleoside-diphosphate reductase M2 chain; Ribonucleotide reductase small chain; ribonucleoside-diphosphate reductase small chain
		Similar to ribonucleotide reductase M2 polypeptide
		Similar to ribonucleotide reductase protein r2 class I
NM_010206 NP_034336.1	F:(C-D)+6.86	receptor
		growth factor receptor
		fibroblast growth factor receptor
		fibroblast growth factor receptor 1
		fibroblast growth factor receptor 1 precursor
		fibroblast growth factor receptor-FLG precursor
		Basic fibroblast growth factor receptor 1
		Basic fibroblast growth factor receptor 1 precursor (FGFR-1) (bFGF-R) (Fms-like tyrosine kinase-2) (c-fgr)
		fibroblast growth factor receptor 1 isoform 1 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
		fibroblast growth factor receptor 1 isoform 2 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Fibroblast Growth Factor Receptor, 3-Ig Domain+2 AA insert; Fibroblast Growth Factor Receptor, 3 Ig-Domain Form
		heparin-binding growth factor receptor
NM_017370 NP_059066.1	F:(IR-D)+6.61	globin
		haptoglobin

		haptoglobin-related protein; Haptoglobin-related locus
		haptoglobin precursor
		Haptoglobin-related protein precursor
		haptoglobin precursor, allele 1
		haptoglobin precursor, allele 2
		Haptoglobin-1 precursor
		Haptoglobin-2 precursor
		haptoglobin alpha 1S
		haptoglobin Hp2
		prohaptoglobin
		preprohaptoglobin
AKO03138 BAB22597.1	F:(IR-D)+5.96	adipose
		a novel adipose specific collagen-like factor, apM1 a novel adipose specific collagen-like factor, apM1 abundant gene transcript 1)
		adiponectin
		Adiponectin precursor (30 kDa adipocyte complement-related protein) (ACRP30) (Adipose most abundant gene transcript 1)(apM-1) (Gelatin-binding protein)
		gelatin-binding protein
		gelatin-binding 28K protein precursor
		adipocyte
		adipocyte-specific secretory protein
NM_007606 NP_031632.1	F:(IR-D)+5.52	anhydrase
		anhydrase, carbonic
		Mol_id: 1; Molecule: Carbonic Anhydrase II; Chain: Null; Synonym: Carbonate Dehydratase, Hca II; Heterogen: Aminocarbonylbenzenesulfonamide
		Mol_id: 1; Molecule: Carbonic Anhydrase II; Chain: Null; Synonym: Carbonate Dehydratase, Hca II; Heterogen: Benzenesulfonamide
		Mol_id: 1; Molecule: Carbonic Anhydrase II; Chain: Null; Synonym: Carbonate Dehydratase, Hca Heterogen: Ethylaminocarbonylbenzenesulfonamide
		carbonic anhydrase II (AA 1-260)
		Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II)
		Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II)(E.C.4.2.1.1) Mutant With Leu 198 Replaced By His(L198H); Replaced By Ala(L198A); Replaced By Arg(L198R)
		Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II) (pH 5.7)
		Carbonic Anhydrase II (Carbonate Dehydratase) (HCA II) (pH 6.5)
		carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase; carbonic anhydrase B

		Carbonic anhydrase II (Carbonate dehydratase II) (CA-II) (Carbonic anhydrase C)
		carbonic anhydrase III
		carbonic anhydrase III, muscle specific
		Carbonic anhydrase III (Carbonate dehydratase III) (CA-III)
		deanhydratase
		carbonate dehydratase
		carbonate dehydratase III
NM_016906 NP_058602.1	F:(C-D)+5.39	Transport protein
		transmembrane channel
		Sec61
		Sec61 alpha form 1; sec61 homolog
		Sec61 alpha form 1
		Sec61 alpha form 2
		Similar to Sec61 alpha form 2
		sec61 homolog
		sec61 homolog
		Similar to CG9539 gene product
NM_025673 NP_079949.1	F:(C-D)+4.22 F:(C-IR)+2.51	Membrane Protein
		Golgi Peripheral Membrane protein
		Golgi protein
		golgi phosphoprotein
		golgi phosphoprotein 3
		golgi phosphoprotein 3 (coat-protein)
		golgi phosphoprotein 3; golgi protein; golgi peripheral membrane protein 1, 34 kDa; golgi-associated protein; coat-protein
		GPP34-related protein
NM_025404 NP_079680.1	F:(IR-D)+4.15	Transport Protein
		Role in Vesicular transport
		ADP-ribosylation
		ADP-ribosylation factor
		ADP ribosylation factor-like protein
		ADP-ribosylation factor 4L
		ADP-ribosylation factor 4-like; ADP-ribosylation factor-like 6; ADP-ribosylation factor-like 7
NM_033037 NP_149026.1	F:(C-D)+3.88	dioxygenase
		cysteine dioxygenase

		cysteine dioxygenase, type I
		Cys dioxygenase I
NM_026853 NP_081129.1	F:(C-IR)+3.77	ankyrin
		ankyrin repeat
		ankyrin repeat and SOCS
		ankyrin repeat and SOCS box-containing protein 5; SOCS box protein ASB-5
		ankyrin repeat and SOCS box-containing 9
		ankyrin repeat and SOCS box-containing protein 11; ankyrin repeat domain-containing SOCS box protein ASB11
		ankyrin repeat and SOCS box-containing protein 13; ankyrin repeat domain-containing SOCS box protein ASB-13
NM_007820 NP_031846.1	F:(C-D)+3.77	oxidase
		Involved in drug metabolism
		nifedipine oxidase
		cytochrome P450 nifedipine oxidase
		cytochrome P450, glucocorticoid-inducible, hepatic
		CP33_HUMAN Cytochrome P450 3A3 (CYP3A3) (HLP)
		Cytochrome P450 3A4 (Quinine 3-monooxygenase) (CYP3A4) (Nifedipine oxidase) (NF-25) (P450-PCN1)
		cytochrome P450, subfamily IIIA, polypeptide 4; nifedipine oxidase; P450-III, steroid inducible; glucocorticoid-inducible P450; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3
		cytochrome P450, family 3, subfamily A, polypeptide 5; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 5; aryl hydrocarbon hydroxylase; xenobiotic monooxygenase; microsomal monooxygenase; flavoprotein-linked monooxygenase; nifedipine oxidase
		Cytochrome P450 3A5 (CYP3A5) (P450-PCN3)
		cytochrome P450 PCN3
AK012765 BAB28453.1	F:(C-D)+3.67 F:(C-IR)+3.16	Dipeptidase Domain (amino acid transport and metabolism)
		Hypothetical protein KIAA0193
		Similar to KIAA0193 gene product
		hypothetical protein BC002980
		Similar to hypothetical protein MGC29406
AJ133523 CAB55352.1	F:(C-D)+3.6 F:(C-IR)+3.48	transferase
		transferase in the Golgi apparatus
		N-Acetylgalactosaminyltransferase
		UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase
		polypeptide N-acetylgalactosaminyltransferase 3; protein-UDP acetylgalactosaminyltransferase

		UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase (GalNAc-T3)
		UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 4 (GalNAc-T4)
		polypeptide N-acetylglucosaminyltransferase 4; UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 4; GalNAc-T4; GalNAc transferase 4; UDP-GalNAc: polypeptide N-acetylglucosaminyltransferase 4; protein-UDP acetylglucosaminyltransferase 4
		UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 6 (GalNAc-T6)
		polypeptide N-acetylglucosaminyltransferase 6; UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 6; UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 6; protein-UDP acetylglucosaminyltransferase 6; GalNAc transferase 6; GalNAc-T6
		UDP-GalNAc-transferase 12
		hypothetical protein FLJ21212; UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 12(GalNAc-T12)
		UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 12
		UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 13
AK020848	F:(C-D)+3.46	monooxygenase
BAB32228.1	F:(C-IR)+2.94	
		cytochrome
		cytochrome P450
		cytochrome P450, family 20
		cytochrome P450, family 20, subfamily A
		Cytochrome P450, family 20, subfamily A, polypeptide 1
		Cytochrome P450, family 20, subfamily A, polypeptide 1, isoform 1
		cytochrome P450 monooxygenase
U89415	F:(C-D)+3.45	elongation factor
AAC36522.1	F:(C-IR)+2.58	
		elongation factor 2
		eukaryotic translation elongation factor 2; polypeptidyl-tRNA translocase; EF-2; eEF2
NM_011817	F:(C-D)+2.52	growth arrest and DNA-damage protein
NP_035947.1	F:(C-IR)+3.43	
		gadd45-related protein
		growth arrest and DNA-damage-inducible, gamma; GADD45-gamma; gadd-related protein
		cytokine responsive protein
AF316872	F:(C-D)+3.41	PTEN putative kinase
AAK28061.1	F:(C-IR)+2.98	
		PTEN induced putative kinase 1; protein kinase BRPK

NM_016661	F:(C-D)+3.36	hydrolase
NP_057870.1	F:(C-IR)+2.64	
		cysteinase
		homocysteinase
		adenosylhomocysteinase
		S-adenosylhomocysteine hydrolase; adenosylhomocysteinase
		S-adenosylhomocysteine hydrolase
		Similar to S-adenosylhomocysteine hydrolase
		S-adenosylhomocysteine hydrolase-like protein
		S-adenosylhomocysteine hydrolase (SAHH), isoform 1
		S-adenosylhomocysteine hydrolase (SAHH), isoform 2
		S-adenosyl homocysteine hydrolase homolog
		S-adenosylhomocysteine hydrolase-like 1
		Similar to S-adenosylhomocysteine hydrolase-like 1
		S-adenosylhomocysteine hydrolase-like 1; S-adenosyl homocysteine hydrolase homolog
		Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)
		similar to Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)
		Putative adenosylhomocysteinase 2 (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)
		Putative adenosylhomocysteinase 3 (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)
NM_013814	F:(C-D)+3.35	transferase
NP_038842.1		
		glycosylation in the Golgi apparatus
		N-Acetylglactosaminyltransferase
		N-acetylglactosaminyltransferase; similar to Q10473 (PID:g1709559)
		polypeptide N-acetylglactosaminyltransferase
		UDP-GalNAc:polypeptide N-acetylglactosaminyl transferase
		polypeptide N-acetylglactosaminyltransferase 1;
		UDP-N-acetyl-alpha-D-galactosamine:polypeptide
		N-acetylglactosaminyltransferase 1; GalNAc-T1; GalNAc transferase 1;
		protein-UDP acetylglactosaminyltransferase 1; UDP-GalNAc:polypeptide
		N-acetylglactosaminyltransferase 1
		polypeptide N-acetylglactosaminyltransferase 2; UDP-GalNAc. transferase 2
		UDP-N-acetyl-alpha-D-galactosamine:polypeptide
		N-acetylglactosaminyltransferase 2 (GalNAc-T2)
		polypeptide N-acetylglactosaminyltransferase 6;
		UDP-N-acetyl-alpha-D-galactosamine:polypeptide
		N-acetylglactosaminyltransferase 6; UDP-GalNAc:polypeptide
		N-acetylglactosaminyltransferase 6; protein-UDP
		acetylglactosaminyltransferase 6; GalNAc transferase 6; GalNAc-T6

NM_023455 NP_075944.1	F:(C-D)+3.32 F:(C-IR)+2.74 F:(IR-D)+2.61	<p>UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase 6 (GalNAc-T6)</p> <p>UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase 13</p> <p>Polypeptide N-acetylglactosaminyltransferase (Protein-UDP acetylglactosaminyltransferase) (UDP-GalNAc:polypeptide, N-acetylglactosaminyltransferase) (GalNAc-T1)</p> <p>transferase</p> <p>N-Acetyltransferase</p> <p>putative N-acetyltransferase</p> <p>putative N-acetyltransferase CML1</p> <p>putative N-acetyltransferase Camello 2</p> <p>N-acetyltransferase 8; kidney- and liver-specific gene; kidney- and liver-specific gene product</p> <p>GLA</p>
NM_025279 NP_079555.1	F:(C-D)+3.32	<p>nuclear protein</p> <p>nuclear ribonucleoprotein</p> <p>RNA-binding protein</p> <p>upregulated nuclear protein</p> <p>transformation upregulated nuclear protein</p> <p>nuclear ribonucleoprotein</p> <p>heterogeneous nuclear ribonucleoprotein</p> <p>heterogeneous nuclear ribonucleoprotein complex K; hnRNP K</p> <p>Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (DC-stretch binding protein) (CSBP) (Transformation upregulated nuclear protein) (TUNP)</p> <p>heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch binding protein; transformation upregulated nuclear protein</p> <p>heterogeneous nuclear ribonucleoprotein K isoform b; dC-stretch binding protein; transformation upregulated nuclear protein</p> <p>nuclear protein</p>
AB035725 BAA88342.1	F:(C-IR)+3.26 F:(C-D)+2.96	<p>nuclear ribonucleoprotein</p> <p>RNA-binding protein</p> <p>heterogeneous nuclear ribonucleoprotein</p> <p>heterogeneous nuclear ribonucleoprotein R</p> <p>hnRNP Q1</p> <p>hnRNP Q2</p> <p>hnRNP Q3</p> <p>NS1 protein</p> <p>NS1-associated protein 1</p>

NM_019709 NP_062683.1	F:(C-D)+3.03	<p>Similar to NS1-associated protein 1</p> <p>NSAP1 protein</p> <p>RNA-binding protein</p> <p>Gry-rbp</p> <p>Similar to apobec-1 complementation factor protease</p>
NM_009108 NP_033134.1	F:(C-D)+3.25	<p>integral membrane ER protein</p> <p>membrane bound transcription factor protease</p> <p>Similar to membrane-bound transcription factor protease, site 1</p> <p>Membrane-bound transcription factor site-1 protease precursor (Site-1 protease) (Subtilisin/kexin-isozyme-1) (SKI-1)</p> <p>site-1 protease preproprotein; site-1 protease (subtilisin-like, sterol-regulated, cleaves sterol regulatory element binding proteins); subtilisin/kexin isozyme-1 preproprotein; KIAA0091</p> <p>nuclear receptor</p> <p>nuclear receptor subfamily 1, group H, member 2</p> <p>nuclear receptor subfamily 1, group H, member 2; ubiquitously-expressed nuclear receptor</p> <p>nuclear receptor subfamily 1, group H, member 3; liver X receptor, alpha</p> <p>Similar to nuclear receptor subfamily 1, group H, member 3</p> <p>nuclear receptor subfamily 1, group H, member 4</p> <p>nuclear orphan receptor LXR-alpha</p> <p>Bile acid receptor</p> <p>farnesol receptor</p> <p>Bile acid receptor (Farnesoid X-activated receptor) (Farnesol receptor HRR-1) (Retinoid X receptor-interacting protein 14) (RXR-interacting protein 14)</p> <p>farnesoid-X-receptor beta splice variant 1</p> <p>farnesoid-X-receptor beta splice variant 2</p> <p>steroid hormone-nuclear receptor NER</p> <p>Ner-I</p> <p>oxysterols receptor</p> <p>Oxysterols receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan receptor LXR-alpha)</p> <p>Oxysterols receptor LXR-beta (Liver X receptor beta) (Nuclear orphan receptor LXR-beta) (Ubiquitously-expressed nuclear receptor) (Nuclear receptor NER)</p>
NM_007611 NP_031637.1	F:(C-D)+3.25 F:(C-IR)+3.1	<p>Protease</p> <p>caspace</p> <p>caspace 7</p>

AK007264 BAB24924.1	F:(C-IR)+3.24	<p> caspace 7, apoptosis-related cysteine protease caspace 7 isoform alpha caspace 7 isoform alpha precursor; ICE-like apoptotic protease 3; apoptotic protease MCH-3; Lice2 alpha/beta/gamma; (ICE-LAP3); (CMH-1) caspace 7 isoform delta caspace 7 isoform delta, large subunit; ICE-like apoptotic protease 3; apoptotic protease MCH-3; Lice2 alpha/beta/gamma Lice2 alpha Lice2 beta cysteine protease Lice2 gamma cysteine protease Mch3 isoform alpha phosphorylase uridine phosphorylase liver-specific uridine phosphorylase Similar to uridine phosphorylase Similar to uridine phosphorylase similar to uridine phosphorylase; similar to Q16831 (PID:g2494059) Uridine phosphorylase (UDRPase) </p>
NM_053069 NP_444299.1	F:(C-D)+3.22	<p> apoptosis specific protein </p>
AK010640 BAC25310.1	F:(C-IR)+3.21	<p> apoptosis-related protein APG5 autophagy 5-like; apoptosis specific protein Protease serine protease prostasin prostasin precursor Prostasin precursor protease, serine, 8 (prostasin) prostasin preproprotein; protease, serine, 8 serine protease protease, serine, 22; brain-specific serine protease 4; protease, serine S1 family member 22; tryptase epsilon Brain-specific serine protease 4 precursor (BSSP-4) (SP001LA) serine protease 27 serine protease PRSS22 marapsin Marapsin precursor marapsin; channel-activating protease 2 pancreasin </p>

NM_019744 NP_062718.1	F:(C-D)+3.19 F:(C-IR)+2.56	<p>nuclear receptor</p> <p>nuclear receptor coactivator</p> <p>Binds and activates androgen receptor</p> <p>nuclear receptor coactivator 4; RET-activating gene ELE1</p> <p>Nuclear receptor coactivator 4 (NCoA-4) (70 kDa androgen receptor coactivator) (70 kDa AR-activator) (Ret-activating protein ELE1); ELE1</p> <p>Similar to nuclear receptor coactivator 4</p> <p>Ref</p> <p>Ret fused gene</p> <p>RET oncogene fusion partner RFG</p> <p>ret/PTC3 chimeric protein</p>
AJ276796 CAC16403.1	F:(C-D)+3.13	<p>synthetase</p> <p>tRNA synthetase</p> <p>cysteinyl-tRNA synthetase</p> <p>Cysteinyl-tRNA synthetase (Cysteine--tRNA ligase) (CysRS)</p> <p>cysteine-tRNA ligase isoform a; cysteine transase; cysteine-tRNA</p>
NM_010421 NP_034551.1	F:(C-IR)+3.12	<p>cysteine-tRNA ligase isoform b; cysteine transase; cysteine-tRNA synthetase</p> <p>cytoplasmic cysteinyl-tRNA synthetase</p> <p>OK/SW-CL.10</p> <p>hexosaminidase</p> <p>hexosaminidase A (alpha polypeptide)</p> <p>hexosaminidase A preproprotein; beta-N-acetylhexosaminidase; N-acetyl-beta-glucosaminidase; lysosomal enzyme beta-N-acetylhexosaminidase A</p> <p>Similar to hexosaminidase A (alpha polypeptide)</p> <p>hexosaminidase B (beta polypeptide)</p> <p>hexosaminidase B preproprotein; N-acetyl-beta-glucosaminidase</p> <p>N-acetyl-alpha-glucosaminidase prepro-polypeptide</p> <p>N-acetyl-beta-glucosaminidase prepro-polypeptide</p> <p>beta-hexosaminidase alpha chain</p> <p>Beta-hexosaminidase alpha chain precursor (N-acetyl-beta-glucosaminidase) (Beta-N-acetylhexosaminidase) (Hexosaminidase A)</p> <p>Beta-hexosaminidase beta chain precursor (N-acetyl-beta-glucosaminidase) (Beta-N-acetylhexosaminidase) (Hexosaminidase B)</p> <p>beta-hexosaminidase beta-subunit</p> <p>beta-N-acetylhexosaminidase alpha chain precursor</p>

AK008434 NP_666245.1	F:(C-IR)+3.08	beta-N-acetylhexosaminidase beta chain precursor cervical cancer proto-oncogene 7 Membrane protein
		peripheral membrane protein Golgi protein golgi phosphoprotein 3; golgi protein; golgi peripheral membrane protein 1, 34 kDa; golgi-associated protein; coat-protein GPP34-related protein
NM_011429 NP_598615.1	F:(C-IR)+3.07	Transport Protein
		component of SNARE complex snapin SNARE associated protein snapin
NM_010847 NP_034977.1	F:(C-D)+3.05	transcription factor
		transcriptional repressor negatively regulates MYC MXI1 gene; max interactor 1 Similar to MAX interacting protein 1 Max-associated protein Mxi1
		MAX interacting protein 1 isoform a; MAX-interacting protein 1; MAX dimerization protein 2 MAX interacting protein 1 isoform b; MAX-interacting protein 1; MAX dimerization protein 2
AK005070 XP_110162	F:(C-D)+2.58 F:(C-IR)+3.04	citrate transporter protein
		mitochondrial citrate transport protein Tricarboxylate transport protein, mitochondrial precursor (Citrate transport protein) (CTP) (Tricarboxylate carrier protein) solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1; solute carrier family 20 (mitochondrial citrate transporter), member 3 citrate transport protein
NM_007484 NP_031510.1	F:(C-D)+3.02	GTPase
		Rho family GTPase ras homolog gene family ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho12; RhoA; Ras homolog gene family, member A (oncogene RHO H12) ras homolog gene family, member B; Aplysia RAS-related homolog 6 (oncogene RHO H6); Aplysia ras-related homolog 6; RhoB; RAS homolog gene family, member B (oncogene RHO H6) ras homolog gene family, member C; Aplysia RAS-related homolog 9 (oncogene RHO H9); Aplysia ras-related homolog 9; RhoC; RAS homolog gene family, member C (oncogene RHO H9)

		<p>Transforming protein RhoA (H12)</p> <p>Transforming protein RhoB (H6)</p> <p>Transforming protein RhoC (H9)</p> <p>ras homolog gene family, member A</p> <p>ras homolog gene family, member C</p> <p>small GTP binding protein RhoA</p> <p>small GTP binding protein RhoB</p> <p>small GTP binding protein RhoC</p> <p>GTPase</p> <p>GTP-binding protein</p> <p>GTP-binding protein rhoA</p> <p>GTP-binding protein rhoB</p> <p>GTP-binding protein rhoC</p> <p>multidrug resistance protein</p> <p>Human RhoA Complexed With Gtp Analogue</p>
NM_019826	F:(C-D)+3.01	dehydrogenase
NP_062800.1	F:(C-IR)+2.55	<p>isovaleryl dehydrogenase</p> <p>isovaleryl-coA dehydrogenase (IVD)</p> <p>Isovaleryl-CoA dehydrogenase, mitochondrial precursor (IVD)</p> <p>isovaleryl-CoA dehydrogenase precursor</p> <p>acyl-CoA dehydrogenase</p> <p>Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor (SCAD) (Butyryl-CoA dehydrogenase)</p> <p>acyl-CoA dehydrogenase precursor, short-chain-specific</p> <p>acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain</p> <p>acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain precursor</p> <p>acyl-Coenzyme A dehydrogenase, short/branched chain precursor</p> <p>medium-chain acyl-CoA dehydrogenase</p> <p>Acyl-CoA dehydrogenase, short/branched chain specific, mitochondrial precursor (SBCAD) (2-methyl branched chain acyl-CoA dehydrogenase) (2-MEBCAD) (2-methylbutyryl-coenzyme A dehydrogenase) (2-methylbutyryl-CoA dehydrogenase)</p>
D63902	F:(C-D)+2.63	transcription factor
BAA09941.1	F:(C-IR)+3	<p>estrogen-responsive finger protein, cfp (RING finger, coiled-coil domains); zinc finger protein 147 (Tripartite motif protein 25)</p> <p>zinc finger protein 147; Zinc finger protein-147; estrogen-responsive finger protein; tripartite motif protein TRIM25; tripartite motif-containing 25</p> <p>Similar to zinc finger protein 147 (estrogen-responsive finger protein)</p>
AF320996	F:(C-D)+2.99	WW domain-containing adapter
AAK73808.1		

NM_008042 NP_032068.1	F:(IR-D)+2.98	<p>WW domain-containing adapter with a coiled-coil region isoform 1</p> <p>WW domain-containing adapter with a coiled-coil region isoform 2</p> <p>WW domain-containing adapter with a coiled-coil region isoform 3</p> <p>A novel protein containing a formin binding protein (FBP28) domain receptor</p> <p>peptide receptor</p> <p>formyl peptide receptor</p> <p>formyl peptide receptor 1; FPR1</p> <p>formyl peptide receptor-like 1; lipoxin A4 receptor (formyl peptide receptor related)</p> <p>FMLP-related receptor</p> <p>FMLP-related receptor I (FMLP-R-I) (Lipoxin A4 receptor) (LXA4 receptor) (RFP) (HM63)</p> <p>FMLP-related receptor II; formyl peptide receptor-like 2</p> <p>RFP=formyl peptide receptor homolog [human, bone marrow, Peptide, 351 aa</p> <p>N-formyl peptide receptor</p> <p>N-formyl peptide receptor-like 2 protein</p> <p>N-formylpeptide receptor fMLP-R26</p> <p>N-formylpeptide receptor fMLP-R98</p> <p>fMet-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor) (FPR) (N-formylpeptide chemoattractant receptor)</p> <p>orphan G-protein coupled receptor Dez isoform a</p> <p>Chemokine receptor-like 1 (G-protein coupled receptor DEZ) (G protein-coupled receptor ChemR23)</p> <p>synthetase</p>
NM_011710 NP_035840.1	F:(C-IR)+2.94	<p>tRNA synthetase</p> <p>Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TRPRS) (IFP53) (hWRS)</p> <p>tryptophanyl-tRNA synthetase; interferon-induced protein 53</p> <p>IFP53</p>
NM_007791 NP_031817.1	F:(C-D)+2.93	<p>regulatory processes important for development and cellular differentiation</p> <p>cysteine rich protein</p> <p>Cysteine-rich protein 1 (CRP1) (CRP)</p> <p>cysteine and glycine rich protein</p> <p>cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain protein</p> <p>Similar to cysteine and glycine-rich protein 1</p> <p>cysteine and glycine-rich protein 2; LIM domain only 5, smooth muscle; SmLIM</p>

NM_054070 NP_473411.1	F:(C-D)+2.9	<p>Smooth muscle cell LIM protein (Cysteine-rich protein 2) (CRP2) (LIM-only protein 5)</p> <p>smooth muscle LIM protein</p> <p>LIM protein MLP</p> <p>cysteine and glycine-rich protein 3 (cardiac LIM protein)</p> <p>cysteine and glycine-rich protein 3; LIM domain only 4 (cardiac LIM protein); cardiac LIM protein; cysteine- and glycine-rich protein 3; cardiac LIM domain protein, cardiac (Muscle LIM protein)</p> <p>myogenic factor LIM3</p> <p>role in mitochondrial protein metabolism</p> <p>paraplegin</p> <p>paraplegin-like protein</p> <p>Paraplegin (Spastic paraplegia protein 7)</p> <p>YME</p> <p>YME1-like 1 (S. cerevisiae)</p> <p>similar to YME1-like 1 (S. cerevisiae)</p> <p>YME1-like 1 isoform 1; ATP-dependent metalloprotease FtsH1 homolog</p> <p>YME1-like 1 isoform 2; ATP-dependent metalloprotease FtsH1 homolog</p> <p>YME1-like 1 isoform 3; ATP-dependent metalloprotease FtsH1 homolog</p> <p>ATP-dependent metalloprotease</p> <p>ATP-dependent metalloprotease FtsH1 homolog</p> <p>FtsH homolog</p> <p>ATP-dependent metalloprotease YME1L</p> <p>AFG3 ATPase family gene</p> <p>AFG3 ATPase family gene 3-like 2; AFG3 (ATPase family gene 3, yeast)-like 2; ATPase family gene 3-like 2; ATPase family gene 3, yeast</p> <p>AFG3-like protein 2</p> <p>Similar to AFG3 ATPase family gene 3-like 2 (yeast)</p>
AK010065 BAB26679.1	F:(C-D)+2.9	<p>putative ATPases</p> <p>dehydrogenase</p> <p>isocitrate dehydrogenase</p> <p>isocitrate dehydrogenase 3</p> <p>isocitrate dehydrogenase 3 (NAD+) alpha</p> <p>isocitrate dehydrogenase 3 (NAD+) alpha precursor; isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial; NAD+-specific ICDH; NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor; isocitrate dehydrogenase (NAD+) alpha chain precursor; H-IDH alpha; isocitric dehydrogenase</p>

		<p>isocitrate dehydrogenase 3, beta subunit isoform a precursor; isocitric dehydrogenase; NAD⁺-specific isocitrate dehydrogenase beta precursor; NAD⁺-specific isocitrate dehydrogenase b subunit; NAD⁺-specific ICDH; isocitrate dehydrogenase, NAD⁽⁺⁾-specific, mitochondrial, beta subunit</p> <p>isocitrate dehydrogenase 3, beta subunit isoform b precursor; isocitric dehydrogenase; NAD⁺-specific isocitrate dehydrogenase beta precursor; NAD⁺-specific isocitrate dehydrogenase b subunit; NAD⁺-specific ICDH; isocitrate dehydrogenase, NAD⁽⁺⁾-specific, mitochondrial, beta subunit</p> <p>isocitrate dehydrogenase 3 (NAD⁺) gamma isoform a precursor; isocitric dehydrogenase; isocitrate dehydrogenase, NAD⁽⁺⁾-specific, mitochondrial, gamma subunit; IDH-gamma; NAD⁺-specific ICDH; NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor</p> <p>isocitrate dehydrogenase 3 (NAD⁺) gamma isoform b precursor; isocitric dehydrogenase; isocitrate dehydrogenase, NAD⁽⁺⁾-specific, mitochondrial, gamma subunit; IDH-gamma; NAD⁺-specific ICDH; NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor</p> <p>Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor</p> <p>Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial precursor (Isocitric dehydrogenase) (NAD⁺-specific ICDH)</p> <p>Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial precursor (Isocitric dehydrogenase) (NAD⁺-specific ICDH)</p> <p>Similar to isocitrate dehydrogenase 3 (NAD⁺) beta</p> <p>NAD⁺-specific isocitrate dehydrogenase beta precursor</p> <p>NAD⁺-specific isocitrate dehydrogenase beta subunit isoform A</p> <p>NAD⁺-specific isocitrate dehydrogenase beta subunit isoform B</p> <p>isocitrate dehydrogenase 3 (NAD⁺) gamma</p>
AK006553 BAB24650.1 NM_025876 NP_080152.1	<p>F:(IR-D)+2.89</p> <p>F:(C-D)+2.88</p>	<p>hypothetical protein FLJ32702</p> <p>kinase</p> <p>CDK5</p> <p>CDK5 regulatory subunit associated protein 1 isoform a; CDK5 activator-binding protein C42-like; chromosome 20 open reading frame 34</p> <p>CDK5 regulatory subunit associated protein 1 isoform b; CDK5 activator-binding protein C42-like; chromosome 20 open reading frame 34</p> <p>CGI-05 protein</p> <p>similar to CGI-05 protein</p> <p>(CGI-05 protein (LOC51654) similar to rat CDK5 activator-binding protein)</p>
NM_023190 NP_075679.1	F:(C-D)+2.87	<p>apoptotic chromatin condensation inducer in the nucleus; acinus</p> <p>acinusL</p> <p>acinusS</p>
NM_008866 NP_032892.1	F:(C-D)+2.86	<p>hydrolase</p> <p>serine hydrolase</p> <p>lysophospholipase</p>

NM_019649 NP_062623.1	F:(C-D)+2.86	lysophospholipase isoform lysophospholipase I; lysophospholipase 1; lysophospholipid-specific lysophospholipase; acyl-protein thioesterase-1 lysophospholipase II; acyl-protein thioesterase similar to lysophospholipase II; acyl-protein thioesterase novel protein similar to lysophospholipase II (LYPLA2) membrane protein
NM_023854 NP_076343.1	F:(C-D)+2.85	transmembrane protein cleft lip and palate transmembrane protein 1 left lip and palate associated transmembrane protein 1 Similar to cleft lip and palate associated transmembrane protein 1 cisplatin(CDDP) resistance related protein CRR cisplatin resistance related protein CRR9p GTPase-activating protein (GAP) interacts with ARF1 ADP-ribosylation factor GTPase activating protein ADP-ribosylation factor GTPase activating protein 3; ADP-ribosylation factor GTPase activating protein 1 zinc finger protein zinc finger protein 289, ID1 regulated; likely ortholog of mouse ZFP289 ARFGAP protein ARFGAP1 protein
NM_008578 NP_032604.1	F:(C-IR)+2.85	transcription factor serum response factor-related protein serum response factor-related protein 2 serum response factor-related protein R2 myocyte-specific enhancer myocyte-specific enhancer factor 2 (XMEF2) MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) box transcription enhancer MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)
NM_009825 NP_033955.1	F:(C-D)+2.83 F:(C-IR)+2.5	colligin colligin-2 collagen binding protein 2

NM_007517 NP_031543.1	F:(C-D)+2.82	<p>serine (or cysteine) proteinase inhibitor, clade H, member 1; collagen-binding protein 1; gp46; colligin-1; collagen-binding protein 2; colligin-2; heat shock protein 47 47 kDa heat shock protein precursor (Collagen-binding protein 1) heat shock protein Hsp47 precursor Collagen-binding protein 2 precursor (Colligin 2) (Rheumatoid arthritis related antigen RA-A47) ancient ubiquitous protein; AUP1; 46 kDa</p>
NM_007434 NP_031460.1	F:(C-D)+2.82	<p>ancient ubiquitous protein AUP1 isoform Ancient ubiquitous protein 1 precursor AUP1 homolog kinase serine/threonine kinase protein serine/threonine kinase rac protein kinase-alpha rac protein kinase-beta RAC-beta serine/threonine protein kinase (RAC-PK-beta) (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta) v-akt murine thymoma viral oncogene homolog 1 serine/threonine protein kinase; Murine thymoma viral (v-akt) oncogene homolog-1 v-akt murine thymoma viral oncogene homolog 2; Murine thymoma viral (v-akt) homolog-2; rac protein kinase beta protein kinase akt1 protein kinase akt2 Akt-3 protein AKT3 protein kinase protein kinase akt3 long splice form protein kinase akt3 short splice form human protein kinase B RAC-alpha serine/threonine kinase (RAC-PK-alpha) (Protein kinase B) (PKB) (C-AKT) protein kinase B gamma RAC-gamma serine/threonine protein kinase (RAC-PK-gamma) (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (STK-2) v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma); protein kinase B gamma protein kinase B gamma 1 peptidase</p>
AK016546 BAB30295.2	F:(C-D)+2.81 F:(C-IR)+2.67	<p>Paper title: Long-lasting antidiabetic effect of a dipeptidyl peptidase 1V-resistant analog of glucagon-like peptide-1.</p>

AK010356 BAB26876.1	F:(C-D)+2.81	<p> dipeptidyl peptidase IV dipeptidyl peptidase IV-related protein-1 dipeptidyl peptidase IV-related protein-2 dipeptidyl peptidase 8 Similar to dipeptidylpeptidase 8 dipeptidyl peptidase 8 isoform 1; dipeptidyl peptidase 8 dipeptidyl peptidase 8 isoform 2; dipeptidyl peptidase 8 dipeptidylpeptidase 9 dipeptidylpeptidase 9; dipeptidyl peptidase 9; dipeptidyl peptidase IV-related protein-2 dipeptidyl peptidase-like protein 9 Def-6 protein </p>
NM_025975 NP_080251.2	F:(C-D)+2.8	<p> differentially expressed in FDCP 6 homolog; differentially expressed in FDCP (mouse homolog) 6 Similar to differentially expressed in FDCP (mouse homolog) 6 t-complex associated testis expressed t-complex associated testis expressed 1 t-complex-associated-testis-expressed 1-like T-complex associated-testis-expressed 1-like (Protein 91/23) Retinitis pigmentosa 3 RP3 candidate gene </p>
AK002807 BAC25007.1	F:(C-D)+2.8 F:(C-IR)+2.71	<p> Protein C20orf29 chromosome 20 open reading frame 29 </p>
NM_008747 NP_032773.1	F:(C-D)+2.8	<p> receptor G-protein coupled receptor mediates neurotensin, such as hypotension, hyperglycemia, hypothermia, antinociception, and regulation of intestinal motility and secretion neurotensin receptor neurotensin receptor 1 Neurotensin receptor type 1 (NT-R-1) (High-affinity levocabastine-insensitive neurotensin receptor) (NTRH) neurotensin receptor 2 neurotensin receptor 2; neurotensin receptor, type 2; levocabastine-sensitive neurotensin receptor; (NT-R-2); (NTR2 receptor) Similar to neurotensin receptor 2 hypothetical protein FLJ20152 </p>
NM_025459 NP_079735.1	F:(C-D)+2.76	

AK003182 BAB22625.1	F:(IR-D)+2.76	<p>motor transport protein</p> <p>ATPase transport protein</p> <p>myosin light chain</p> <p>myosin alkali light chain, slow skeletal muscle</p> <p>atrial/embryonic alkali myosin light chain; myosin, atrial/fetal muscle, light chain</p> <p>embryonic myosin alkali light chain (MLC1)</p> <p>embryonic/atrial myosin light chain (MLC-1-emb/A isoform)</p> <p>Myosin light chain 1, embryonic muscle/atrial isoform (PRO1957)</p> <p>myosin light chain-1</p> <p>ventricular myosin L1</p> <p>cardiac myosin light chain-1</p> <p>myosin light chain 1 slow</p> <p>myosin alkali light chain 1 slow a; (MLC1sa); myosin light chain 1, slow-twitch muscle A isoform</p> <p>Myosin light chain 1, slow-twitch muscle B/ventricular isoform (MLC1SB) (Alkali)</p> <p>myosin alkali L 1Sb</p> <p>MLC-1V/Sb isoform</p> <p>fast myosin alkali light chain 1</p> <p>Similar to myosin, light polypeptide 1, alkali; skeletal, fast</p> <p>myosin alkali light chain 1, fast skeletal muscle, form 1</p> <p>Myosin light chain 1, skeletal muscle isoform (MLC1F) (A1 catalytic) (Alkali)</p> <p>fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2 catalytic</p> <p>myosin alkali light chain 1, fast skeletal muscle, form 2</p> <p>fast skeletal myosin alkali light chain 1 isoform 3f; A1 catalytic; A2 catalytic</p> <p>myosin light chain 3</p> <p>myosin alkali light chain 3, ventricular and slow skeletal muscle</p> <p>myosin, light polypeptide 3, alkali; ventricular, skeletal, slow</p> <p>Myosin light chain 3, skeletal muscle isoform (A2 catalytic) (Alkali) (MLC3F)</p> <p>myosin alkali L 3F</p> <p>myosin, light polypeptide 4, alkali; atrial, embryonic</p> <p>myosin alkali light chain 4, embryonic and atrial</p>
NM_013771 NP_038799.1	F:(C-IR)+2.75	<p>role in mitochondrial protein metabolism</p> <p>ATP-dependent metalloprotease YME1L</p> <p>ATP-dependent metalloprotease FtsH1 homolog</p>

<p>NM_016774 NP_058054.1</p>	<p>F:(C-D)+2.74</p>	<p>YME1-like 1 (S. cerevisiae) Similar to YME1-like 1 (S. cerevisiae) YME1-like 1 isoform 1; ATP-dependent metalloprotease FtsH1 homolog YME1-like 1 isoform 2; ATP-dependent metalloprotease FtsH1 homolog YME1-like 1 isoform 3; ATP-dependent metalloprotease FtsH1 homolog ATPase putative ATPases AFG3 ATPase family gene 3-like 2; AFG3 (ATPase family gene 3, yeast)-like 2; ATPase family gene 3-like 2; ATPase family gene 3, yeast Similar to AFG3 ATPase family gene 3-like 2 (yeast) paraplegin paraplegin-like protein ATP synthase H⁺-transporting two-sector ATPase beta chain precursor, mitochondrial ATPase, H⁺ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1; ATPase, H⁺ transporting, lysosomal, beta polypeptide, 58kD; vacuolar proton pump, subunit 3; vacuolar ATP synthase subunit B, kidney isoform; V-ATPase B1 subunit; endomembrane proton pump 58 kDa subunit; H(+)-transporting two-sector ATPase, 58kD subunit; H⁺-ATPase beta 1 subunit; ATPase, H⁺ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1 (Renal tubular acidosis with deafness) ATP synthase, H⁺ transporting, mitochondrial F1 complex, beta polypeptide; ATP synthase, H⁺ transporting, mitochondria F1 complex, beta Similar to ATP synthase, H⁺ transporting, mitochondrial F1 complex, beta polypeptide ATPase beta, F1 F1 beta subunit put. F1-beta precursor transport protein amino acid transport protein LAT1 protein L-type amino acid transporter subunit L-type amino acid transporter 1 Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 light chain) (4F2 LC) (4F2LC) (CD98 light chain) (Integral membrane protein E16) (hLAT1) sodium-independent neutral amino acid transporter LAT1 L-type amino acid transporter 2; LAT-2 Large neutral amino acids transporter small subunit 2 (L-type amino acid transporter 2) (hLAT2) glycoprotein-associated amino acid transporter LAT2</p>
<p>NM_016972 NP_058668.1</p>	<p>F:(C-IR)+2.73</p>	<p>YME1-like 1 (S. cerevisiae) Similar to YME1-like 1 (S. cerevisiae) YME1-like 1 isoform 1; ATP-dependent metalloprotease FtsH1 homolog YME1-like 1 isoform 2; ATP-dependent metalloprotease FtsH1 homolog YME1-like 1 isoform 3; ATP-dependent metalloprotease FtsH1 homolog ATPase putative ATPases AFG3 ATPase family gene 3-like 2; AFG3 (ATPase family gene 3, yeast)-like 2; ATPase family gene 3-like 2; ATPase family gene 3, yeast Similar to AFG3 ATPase family gene 3-like 2 (yeast) paraplegin paraplegin-like protein ATP synthase H⁺-transporting two-sector ATPase beta chain precursor, mitochondrial ATPase, H⁺ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1; ATPase, H⁺ transporting, lysosomal, beta polypeptide, 58kD; vacuolar proton pump, subunit 3; vacuolar ATP synthase subunit B, kidney isoform; V-ATPase B1 subunit; endomembrane proton pump 58 kDa subunit; H(+)-transporting two-sector ATPase, 58kD subunit; H⁺-ATPase beta 1 subunit; ATPase, H⁺ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1 (Renal tubular acidosis with deafness) ATP synthase, H⁺ transporting, mitochondrial F1 complex, beta polypeptide; ATP synthase, H⁺ transporting, mitochondria F1 complex, beta Similar to ATP synthase, H⁺ transporting, mitochondrial F1 complex, beta polypeptide ATPase beta, F1 F1 beta subunit put. F1-beta precursor transport protein amino acid transport protein LAT1 protein L-type amino acid transporter subunit L-type amino acid transporter 1 Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 light chain) (4F2 LC) (4F2LC) (CD98 light chain) (Integral membrane protein E16) (hLAT1) sodium-independent neutral amino acid transporter LAT1 L-type amino acid transporter 2; LAT-2 Large neutral amino acids transporter small subunit 2 (L-type amino acid transporter 2) (hLAT2) glycoprotein-associated amino acid transporter LAT2</p>

NM_008492 NP_032518.1	F:(C-IR)+2.73	<p>solute carrier</p> <p>solute carrier family 7</p> <p>similar to solute carrier family 7</p> <p>solute carrier family 7 (cationic amino acid transporter, y⁺ system), member 5; Membrane protein E16; Solute carrier family 7, member 5; 4F2 light chain</p> <p>Similar to solute carrier family 7 (cationic amino acid transporter, y⁺ system), member 5</p> <p>solute carrier family 7 (cationic amino acid transporter, y⁺ system), member 8</p> <p>solute carrier family 7, member 10; asc-type amino acid transporter 1</p> <p>CD98</p> <p>CD98 light chain</p> <p>dehydrogenase</p> <p>lactate dehydrogenase</p> <p>lactate dehydrogenase A</p> <p>L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M)</p> <p>lactate dehydrogenase A-like</p> <p>L-lactate dehydrogenase A-like</p> <p>lactate dehydrogenase B</p> <p>L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H)</p> <p>lactate dehydrogenase C</p> <p>L-lactate dehydrogenase C chain (LDH-C) (LDH testis subunit) (LDH-X)</p> <p>L-lactate dehydrogenase chain H</p> <p>L-lactate dehydrogenase chain M</p> <p>L-lactate dehydrogenase chain X</p>
AK010325 NP_542123.1	F:(C-D)+2.72 F:(C-IR)+2.78	<p>transmembrane</p> <p>transmembrane 9</p> <p>transmembrane 9 superfamily member 1</p> <p>transmembrane 9 superfamily member 1; multispanning membrane protein (70kD); transmembrane protein 9 superfamily member 1</p> <p>transmembrane 9 superfamily member 2; p76</p> <p>transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2</p> <p>Transmembrane 9 superfamily protein member 2 precursor (p76)</p> <p>transmembrane 9 superfamily member 3</p> <p>transmembrane protein TM9SF3</p> <p>Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-iso)</p> <p>Transmembrane 9 superfamily protein member 4</p>

AK005989 BAB24354.1	F:(C-D)+2.72	<p>binding protein</p> <p>SM-11044 binding protein</p> <p>Similar to <i>S.cerevisiae</i> EMP70 protein precursor (S25110)</p> <p>isomerase</p> <p>protein disulfide isomerase protein</p> <p>protein disulfide isomerase-related protein</p> <p>protein disulfide isomerase-related protein 5</p> <p>Protein disulfide isomerase A6 precursor (Protein disulfide isomerase P5)</p> <p>human P5</p> <p>P5 protein precursor</p>
NM_019973 NP_064357.1	F:(C-D)+2.72 F:(C-IR)+2.64	<p>binding protein</p> <p>DNA binding protein</p> <p>negative regulatory element-binding protein; NREBP</p> <p>SON protein (SON3) (Negative regulatory element-binding protein) (NRE-binding protein) (DBP-5) (Bax antagonist selected in <i>saccharomyces</i> 1) (BASS1) (Protein C21orf50)</p> <p>SON DNA-binding protein isoform B; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in <i>Saccharomyces</i> 1</p> <p>SON DNA-binding protein isoform C; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in <i>Saccharomyces</i> 1</p> <p>SON DNA-binding protein isoform E; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in <i>Saccharomyces</i> 1</p> <p>SON DNA-binding protein isoform F; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in <i>Saccharomyces</i> 1</p> <p>SON DNA-binding protein isoform G; NRE-binding protein; chromosome 21 open reading frame 50; SON protein; negative regulatory element-binding protein; Bax antagonist selected in <i>Saccharomyces</i> 1</p>
AK004564 BAB23375.1 NM_011177 NP_035307.1	F:(C-D)+2.71 F:(C-IR)+2.71	<p>Similar to RIKEN cDNA 1200003G01 gene</p> <p>protease</p> <p>serine protease</p> <p>kallikrein serine protease</p> <p>protease M</p> <p>kallikrein-like serine protease; zyme; protease M; neurosin</p> <p>kallikrein 6 (neurosin, zyme)</p> <p>kallikrein-like protein 6</p> <p>kallikrein 6 preproprotein; protease M; protease, serine, 9; neurosin; zyme</p> <p>Kallikrein 6 precursor (Protease M) (Neurosin) (Zyme) (SP59)</p>

Y00769
CAA68738.1

F:(C-D)+2.71

kallikrein 8 isoform 1 preproprotein; protease, serine, 19; neuropsin; ovasin;
tumor-associated differentially expressed gene 14
kallikrein 8 isoform 2; protease, serine, 19; neuropsin; ovasin;
tumor-associated differentially expressed gene 14
kallikrein 14
kallikrein 14 preproprotein; kallikrein-like protein 6
Kallikrein 14 precursor (Kallikrein-like protein 6) (KLK-L6)
KLK15
Kallikrein 15 precursor (ACO protease)
kallikrein 15 isoform 4 preproprotein; ACO protease; prostinoge
kallikrein-like serine protease
prostinogen
protease
serine protease
serine protease ovasin
serine protease TADG14; (Tumor-associated differentially expressed
gene-14 protein)
neuropsin
neuropsin type
Neuropsin precursor (NP) (Kallikrein 8) (Ovasin) (Serine protease
TADG-14) (Tumor-associated differentially expressed gene-14 protein)
neuropsin type2
protease
ACO protease
membrane receptor
integrin
integrin beta 1
Integrin beta-1 precursor (Fibronectin receptor beta subunit) (CD29 antigen)
(Integrin VLA-4 beta subunit)
integrin beta 1 isoform 1A
integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit;
fibronectin receptor beta subunit
integrin beta 1 isoform 1B
integrin beta 1 isoform 1B precursor; integrin VLA-4 beta subunit;
fibronectin receptor beta subunit
integrin beta 1 isoform 1C
integrin beta 1 isoform 1C-1 precursor; integrin VLA-4 beta subunit;
fibronectin receptor beta subunit
integrin beta 1 isoform 1C-2 precursor; integrin VLA-4 beta
subunit; fibronectin receptor beta subunit
integrin beta 1 isoform 1D

<p>NM_007614 NP_031640.1</p>	<p>F:(C-D)+2.7 F:(C-IR)+2.75</p>	<p>integrin beta 1 isoform 1D precursor; integrin VLA-4 beta subunit; fibronectin receptor beta subunit fibronectin receptor beta chain precursor integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) integrin beta-2 subunit Integrin beta-2 precursor (Cell surface adhesion glycoproteins LFA-1/CR3/p150,95 beta-subunit) (CD18) (Complement receptor C3 beta-subunit) leukocyte adhesion protein beta chain (CD18) precursor integrin beta chain, beta 2 precursor; Integrin, beta-2 (antigen CD18 (p95), lymphocyte function-associated; cell surface adhesion glycoprotein (LFA-1/CR3/P150,959 beta subunit precursor) integrin, beta 7 integrin beta-7 subunit integrin beta-7 chain precursor cadherin-associated protein</p>
<p>NM_007779 NP_031805.1</p>	<p>F:(C-D)+2.7</p>	<p>beta-catenin Beta-catenin (PRO2286) globin plakoglobin plakoglobin, desmosomal junction plakoglobin Junction plakoglobin (Desmoplakin III) junction plakoglobin isoform 1; gamma-catenin Receptor Colony stimulating factor 1 receptor, precursor colony stimulating factor 1 receptor precursor; (CSF-1-R); FMS proto-oncogene; (c-fms); CD115 antigen; macrophage colony stimulating factor I receptor; similar to mouse Friend murine leukemia virus integration site 2 put. c-fms precursor KIT protein mast/stem cell growth factor receptor Mast/stem cell growth factor receptor precursor (SCFR) (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen) protein-tyrosine kinase, receptor type kit precursor v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog precursor platelet-derived growth factor receptor alpha precursor Alpha platelet-derived growth factor receptor precursor (PDGF-R-alpha) (CD140a antigen)</p>

NM_007415 NP_031441.2	F:(C-D)+2.7	<p>Beta platelet-derived growth factor receptor precursor (PDGF-R-beta) (CD140b antigen)</p> <p>platelet-derived growth factor receptor</p> <p>platelet-derived growth factor A receptor</p> <p>platelet-derived growth factor receptor A chain</p> <p>alpha-platelet-derived growth factor receptor</p> <p>platelet-derived growth factor receptor, beta polypeptide</p> <p>protein p145-ckit (AA 1 - 976)</p> <p>FLT3 receptor tyrosine kinase</p> <p>transferase</p>
NM_025808 NP_080084.2	F:(C-D)+2.69 F:(C-IR)+3.14	<p>poly(ADP-ribosyl)transferase</p> <p>may participate in the pathophysiology of type I diabetes</p> <p>ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)</p> <p>ADP-ribosyltransferase (NAD+; poly(ADP-ribose) polymerase)-like 2</p> <p>poly(ADP-ribosyl)transferase; ADP-ribosyltransferase NAD(+); poly(ADP-ribose) synthetase</p> <p>Poly [ADP-ribose] polymerase-1 (PARP-1) (ADPRT) (NAD(+)</p> <p>ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1)</p> <p>Poly [ADP-ribose] polymerase-2 (PARP-2) (NAD(+)</p> <p>ADP-ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (pADPRT-2) (hPARP-2)</p> <p>similar to Poly [ADP-ribose] polymerase-1 (PARP-1) (ADPRT) (NAD(+)</p> <p>ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1)</p> <p>NAD+ ADP-ribosyltransferase</p> <p>NAD ADP-ribosyltransferase, nuclear</p> <p>Transcription factor</p>
NM_025939 NP_080215.1	F:(C-D)+2.52 F:(C-IR)+2.69	<p>DNA binding transcription factor</p> <p>leucine-zipper transcriptional regulator; LZTR</p> <p>LZTR-1</p> <p>leucine-zipper-like transcriptional regulator, 1; Leucine-zipper-like regulator-1</p> <p>carboxylase</p> <p>participates in de novo purine nucleotide synthesis</p> <p>phosphoribosylaminoimidazole carboxylase;</p> <p>phosphoribosylaminoimidazole carboxylase,</p> <p>phosphoribosylaminoribosylaminoimidazole succinocarboxamide synthetase; AIR carboxylase; SAICAR synthetase</p> <p>Multifunctional protein ADE2 [Includes:</p> <p>Phosphoribosylaminoimidazole-succinocarboxamide synthase (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (AIR carboxylase) (AIRC)]</p> <p>multifunctional purine biosynthesis protein</p>

NM_010123 NP_034253.1	F:(C-IR)+2.69	<p>multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase)</p> <p>translation initiation factor</p> <p>translation initiation factor 3</p> <p>translation initiation factor 3 large subunit</p> <p>Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (eIF3 p167) (eIF3 p180) (eIF3 p185) (eIF3a)</p> <p>eukaryotic translation initiation factor 3, subunit 10 theta, 50/170kDa; eukaryotic translation initiation factor 3, subunit 10 (theta, 170kD); Eukaryotic translation initiation factor 3, subunit 10, 170kD; eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD)</p> <p>p167</p>
NM_011225 NP_035355.1	F:(C-D)+2.67	<p>GTPase</p> <p>RAB18</p> <p>RAB18, member RAS oncogene family; RAB18 small GTPase</p> <p>Ras-related protein Rab-18; ras-related protein 18</p> <p>ras-related small GTPase RAB18</p>
NM_010068 NP_034198.1	F:(C-IR)+2.67	<p>transferase</p> <p>methyltransferase</p> <p>cytosine methyltransferase</p> <p>function in de novo methylation of DNA</p> <p>DNA cytosine methyltransferase 3 alpha</p> <p>DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase HsaIIIA) (DNA MTase HsaIIIA) (M.HsaIIIA)</p> <p>DNA cytosine methyltransferase 3 alpha isoform a; DNA methyltransferase HsaIIIA; DNA MTase HsaIIIA; DNA cytosine methyltransferase 3A2</p> <p>DNA cytosine methyltransferase 3 alpha isoform b; DNA methyltransferase HsaIIIA; DNA MTase HsaIIIA; DNA cytosine methyltransferase 3A2</p> <p>DNA cytosine methyltransferase 3A2</p> <p>DNA cytosine methyltransferase 3 beta</p> <p>DNA (cytosine-5)-methyltransferase 3B (Dnmt3b) (DNA methyltransferase HsaIIIB) (DNA MTase HsaIIIB) (M.HsaIIIB)</p> <p>DNA cytosine-5 methyltransferase 3 beta isoform 1; DNA methyltransferase HsaIIIB; DNA MTase HsaIIIB</p> <p>DNA cytosine-5 methyltransferase 3 beta isoform 2; DNA methyltransferase HsaIIIB; DNA MTase HsaIIIB</p> <p>cytosine-5-methyltransferase 3-like protein isoform 2;</p> <p>cytosine-5-methyltransferase 3-like protein; human</p> <p>cytosine-5-methyltransferase 3-like protein</p> <p>DNA cytosine-5 methyltransferase 3 beta isoform 3; DNA methyltransferase HsaIIIB; DNA MTase HsaIIIB</p> <p>DNA cytosine-5 methyltransferase 3 beta isoform 6; DNA methyltransferase HsaIIIB; DNA MTase HsaIIIB</p>

NM_008732 NP_032758.1	F:(C-D)+2.65	<p>DNA cytosine-5 methyltransferase 3 beta 3</p> <p>DNA methyltransferase 3 beta 5</p> <p>Membrane protein</p> <p>integral membrane protein</p> <p>Transport protein</p> <p>proton-coupled divalent metal ion transporters</p> <p>integral membrane protein</p> <p>Nramp; Natural resistance-associated macrophage protein</p> <p>Natural resistance-associated macrophage protein 1 (NRAMP 1)</p> <p>NRAMP2; natural resistance-associated macrophage protein 2; (Divalent metal transporter 1) (DMT1); NRAMP2 iron transporter</p> <p>natural resistance-associated macrophage protein 2 non-IRE form</p> <p>solute carrier</p> <p>solute carrier family 11</p> <p>solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; natural resistance-associated macrophage protein 1 (might include Leishmaniasis); solute carrier family 11 (sodium/phosphate symporters), member 1</p> <p>solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2; natural resistance-associated macrophage protein 2</p>
NM_013506 NP_038534.1	F:(C-IR)+2.65	<p>translation initiation factor</p> <p>initiation factor 4</p> <p>initiation factor 4A</p> <p>Eukaryotic initiation factor 4A-like NUK-34</p> <p>translation initiation factor eIF-4A-I; eukaryotic translation initiation factor 4A, isoform 1; (eIF-4A-I) (eIF4A-I)</p> <p>Similar to eukaryotic translation initiation factor 4A, isoform 1</p> <p>Eukaryotic initiation factor 4A-II; eukaryotic translation initiation factor 4A, isoform 2</p> <p>translation initiation factor eIF-4A2 homolog</p>
NM_013512 NP_038540.1	F:(C-D)+2.64	<p>BM-010</p> <p>phosphatase</p> <p>protein-tyrosine phosphatase</p> <p>erythrocyte protein band 4.1-like 4</p> <p>Similar to erythrocyte protein band 4.1-like 4</p> <p>erythrocyte membrane protein band 4.1 like 4B; EHM2 gene;</p> <p>FERM-containing protein</p> <p>protein-tyrosine phosphatase</p> <p>protein tyrosine phosphatase, non-receptor type 4; megakaryocyte phosphatase; PTPase-MEG1; protein tyrosine phosphatase MEG1; megakaryocyte protein-tyrosine phosphatase</p>

NM_010050 NP_034180.1	F:(C-D)+2.64	Protein tyrosine phosphatase, non-receptor type 4 (Protein-tyrosine phosphatase MEG1) (PTPase-MEG1) (MEG) hNBL4 deiodinase
NM_009010 NP_033036.1	F:(C-D)+2.64	iodothyronine deiodinase type 2 iodothyronine deiodinase; (Type-II 5'deiodinase) (DIOII) (Type 2 DI) (SDII) nucleotide excision repair human RAD23A homolog similar to <i>S.cerevisiae</i> RAD23 RAD23 homolog A (<i>S. cerevisiae</i>) Similar to RAD23 (<i>S. cerevisiae</i>) homolog A RAD23 homolog B (<i>S. cerevisiae</i>) RAD23 protein homolog2 UV excision repair protein RAD23 homolog A; RAD23, yeast homolog, A; RAD23 homolog A UV excision repair protein RAD23 homolog A (HHR23A) HHR23A protein UV excision repair protein RAD23 homolog B (HHR23B) (XP-C repair complementing complex 58 kDa protein) (P58) similar to UV excision repair protein RAD23 homolog B (HHR23B) (XP-C repair complementing complex 58 kDa protein) (P58)
NM_008218 NP_032244.1	F:(C-IR)+2.64 F:(IR-D)+2.99	Transport protein Oxygen transport Hemoglobin alpha globin hemoglobin alpha-1 globin chain hba1 alpha globin HBA1 hemoglobin, alpha 2 hba2 alpha globin HBA2
AK006835 NP_694878.1	F:(C-D)+2.63	Transcription factor transcription repressor HMG box containing protein 1 HMG box-containing protein 1a
NM_009477 NP_033503.1	F:(IR-D)+2.63	phosphorylase Upase

NM_011340 NP_035470.1	F:(C-D)+2.62	<p>uridine phosphorylase; (UDRPase) liver-specific uridine phosphorylase similar to uridine phosphorylase; similar to Q16831 (PID:g2494059) neurotrophic and antiangiogenic serpin</p> <p>Proliferative Diabetic Retinopathy is Associated with a Low Level of the Natural Ocular Anti-angiogenic Agent Pigment Epithelium-derived Factor (PEDF) in Aqueous Humor pigment epithelial-differentiating factor pigment epithelial-differentiating factor precursor pigment epithelium-derived factor Pigment epithelium-derived factor precursor (PEDF) (EPC-1) proteinase inhibitor serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1; pigment epithelium-derived factor serine proteinase inhibitor homolog EPC-1</p>
NM_009128 NP_033154.1	F:(C-D)+2.62	<p>Similar to serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 membrane protein</p> <p>integral membrane protein stearoyl-CoA desaturase (delta-9-desaturase) Acyl-CoA desaturase (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase) similar to stearoyl-CoA desaturase PRO0998</p>
AI156588 XP_125732	F:(C-D)+2.61	<p>acetolactate</p> <p>acetolactate synthase ilvB (bacterial acetolactate synthase)-like isoform 1; acetolactate synthase homolog</p>
NM_008160 NP_032186.1	F:(C-D)+2.6	<p>peroxidase</p> <p>glutathione peroxidase activity were significantly decreased in Type II diabetics—"Antioxidant status and lipid peroxidation in type II diabetes mellitus." glutathione peroxidase glutathione peroxidase 1; (GSHPx-1) (Cellular glutathione peroxidase) similar to glutathione peroxidase 1 glutathione peroxidase-GI glutathione peroxidase 2</p>

NM_009318 NP_033344.1	F:(IR-D)+2.59	<p>Glutathione peroxidase-gastrointestinal (GSHPx-GI) (Glutathione peroxidase-related protein 2) (Gastrointestinal glutathione peroxidase) (GPRP)</p> <p>gastrointestinal glutathione peroxidase</p> <p>gastrointestinal glutathione peroxidase 2</p> <p>opal codon coding for selenocysteine</p> <p>Membrane protein</p> <p>transmembrane protein</p> <p>transmembrane glycoprotein</p> <p>Mediates interactions with MHC Class 1 and TAP molecules</p> <p>tapasin</p> <p>Tapasin*01</p> <p>Tapasin*02</p> <p>Tapasin precursor (TPSN) (TPN) (TAP-binding protein) (TAP-associated protein) (NGS-17)</p> <p>TAP-binding protein (tapasin), isoform 1</p> <p>tapasin isoform 1 precursor; TAP-binding protein; TAP-associated protein</p> <p>TAP-binding protein (tapasin), isoform 2</p> <p>tapasin isoform 2 precursor; TAP-binding protein; TAP-associated protein</p> <p>TAP-binding protein (tapasin), isoform 3</p> <p>tapasin isoform 3 precursor; TAP-binding protein; TAP-associated</p> <p>TAP-associated protein, TAP-A</p> <p>tapasinas</p>
NM_022331 NP_071726.1	F:(C-IR)+2.58	<p>homocysteine</p> <p>homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1; MMS-inducible gene</p> <p>Similar to homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1</p> <p>Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein (Methyl methanesulfonate (MMS)-inducible fragment protein 1)</p> <p>stress protein Herp</p>
NM_022417 NP_071862.1	F:(C-D)+2.58 F:(C-IR)+2.6	<p>membrane protein</p> <p>Integral membrane protein</p> <p>Integral membrane protein 2C (Transmembrane protein BRI3) (NPD018)</p> <p>integral membrane protein 3; E25 protein</p> <p>Similar to integral membrane protein 3</p> <p>BRI3</p> <p>NPD018</p>

NM_011829 NP_035959.1	F:(C-D)+2.57	<p>cerebral protein-14</p> <p>cerebral protein</p> <p>dehydrogenase</p> <p>inosine monophosphate; (IMP)</p> <p>IMP dehydrogenase; inosine-5'-monophosphate dehydrogenase</p> <p>IMP dehydrogenase I</p> <p>similar to IMP dehydrogenase I</p> <p>Inosine-5'-monophosphate dehydrogenase 1 (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1)</p> <p>similar to Inosine-5-monophosphate dehydrogenase 1 (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1)</p> <p>IMP dehydrogenase II</p> <p>Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2) (IMPDH-II) (IMPD 2)</p>
NM_023719 NP_076208.1	F:(C-IR)+2.57	<p>VDUP1</p> <p>brain-expressed HHCPA.78 homolog VDUP1</p> <p>dihydroxyvitamin</p> <p>dihydroxyvitamin D3-induced protein</p> <p>thioredoxin interacting protein; upregulated by 1,25-dihydroxyvitamin D-3</p>
NM_018868 NP_061356.1	F:(C-D)+2.57	<p>nucleolar protein</p> <p>nucleolar protein NOP5/NOP58; (Nucleolar protein 5) (NOP58) (HSPC120)</p> <p>Nucleolar protein Nop56 (Nucleolar protein 5A); hNop56</p> <p>HSPC120</p>
NM_016741 NP_058021.1	F:(C-IR)+2.57	<p>receptor</p> <p>receptor in platelets</p> <p>receptor for thrombospondin and collagen in platelets, important role in cell adhesion</p> <p>CLA-1</p> <p>membrane glycoprotein CLA-1 protein long form precursor</p> <p>CD36 antigen</p> <p>cell adhesion receptor CD36</p> <p>CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36 antigen (collagen type I); cluster determinant 36; fatty acid translocase; scavenger receptor class B, member 3</p> <p>Similar to CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1</p> <p>scavenger receptor class B, member 1; CD36 antigen-like 1; scavenger receptor class B type 1; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1</p>

<p>NM_011571 NP_035701.1</p>	<p>F:(C-D)+2.56</p>	<p>scavenger receptor class B, member 2; CD36 antigen (collagen type I receptor, thrombospondin receptor) -; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) lysosomal integral membrane protein II Lysosome membrane protein II (LIMP II) (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) 85kDa lysosomal sialoglycoprotein glycoprotein GPIIb/GPIV Platelet glycoprotein IV (GPIV) (GPIIb) (CD36 antigen) (PAS IV) (PAS-4 protein) Kinase</p>
<p>NM_010587 NP_034717.1</p>	<p>F:(C-D)+2.56</p>	<p>protein kinase serine/threonine protein kinase Testis-specific protein kinase 1 (Testicular protein kinase 1); TESK1 Similar to testis-specific kinase 1 Testis-specific protein kinase 2 testicular protein kinase 2 scaffold protein</p>
<p>NM_007399 NP_031425.1</p>	<p>F:(C-IR)+2.55</p>	<p>general endocytosis intersectin 1 (SH3 domain protein); SH3 domain protein-1A; intersectin (SH3 domain protein 1A); human intersectin-SH3 domain-containing protein SH3P17 intersectin short form intersectin long isoform Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein) intersectin 2 long isoform intersectin 2 isoform 1; SH3 domain protein 1B; SH3P18-like WASP associated protein intersectin 2 isoform 3; SH3 domain protein 1B; SH3P18-like WASP associated protein protease and adhesion domains membrane-anchored protein disintegrin disintegrin-metalloprotease MADM a disintegrin and metalloprotease domain 10; ADAM10 ADAM 17 precursor (A disintegrin and metalloproteinase domain 17) (TNF-alpha converting enzyme) (TNF-alpha convertase) (Snake venom-like protease) (CD156b antigen)</p>

NM_025827 NP_080103.1	F:(C-D)+2.54	a disintegrin and metalloproteinase domain 17 isoform 1 preproprotein; TNF-alpha converting enzyme; snake venom-like protease a disintegrin and metalloproteinase domain 17 isoform 2 preproprotein; TNF-alpha converting enzyme; snake venom-like protease TNF-alpha converting enzyme TNF-alpha converting enzyme precursor protease
NM_016696 NP_057905.1	F:(C-D)+2.54	ATP dependent protease mitochondrial matrix protein LON protease Lon protease-like protein peroxisomal lon protease endopeptidase La homolog precursor, mitochondrial (version 1) endopeptidase La homolog precursor, mitochondrial (version 2) ATP-dependent lon protease protease, serine, 15; Lon protease-like protein; hLON ATP-dependent protease; LON protease Lon protease homolog, mitochondrial precursor (Lon protease-like protein) (LONP) (LONHs) protease, serine, 15
NM_016696 NP_057905.1	F:(C-D)+2.54	heparan sulfate proteoglycans glypican glypican 1 precursor; GPC1 Glypican 2 glypican 2; cerebroglycan glypican 4 similar to glypican 4 Glypican-4 precursor (K-glypican) glypican-6 glypican 6 precursor; GPC6 proteoglycan heparan sulfate proteoglycan
NM_010028 NP_034158.1	F:(C-D)+2.54	helicase protein ATP-dependent RNA helicase helicase like protein 2 DEAD box RNA helicase DDX4 protein DEAD box RNA helicase DDX3

		<p>DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3</p> <p>DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3; DEAD/H box-3; helicase like protein 2; CAP-Rf</p> <p>DEAD-box protein 3 (Helicase-like protein 2) (HLP2) (DEAD-box, X isoform)</p> <p>similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3; D-E-A-D (aspartate-glutamate-alanine-aspartate) box polypeptide 3; DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 3; embryonic RNA helicase [<i>Mus musculus</i>]</p> <p>DEAD-box protein 3, Y-chromosomal</p> <p>DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome; DEAD/H box-3, Y-linked</p> <p>dead box, Y isoform</p> <p>dead box, X isoform</p> <p>DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 4; VASA protein</p> <p>VASA protein</p> <p>DEAD-box protein 4 (VASA homolog)</p> <p>DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD)</p> <p>DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 isoform 1; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD); probable RNA-dependent helicase p72</p> <p>Probable RNA-dependent helicase p72 (DEAD-box protein p72) (DEAD-box protein 17)</p> <p>DEAD-box protein p72</p> <p>HSPC288</p> <p>Protein C14orf1 (HSPC288) (Protein AD-011) (x0006)</p> <p>potential membrane protein C14orf1</p> <p>dehydrogenase</p> <p>retinol dehydrogenase</p> <p>sterol/retinol dehydrogenase</p> <p>retinol dehydrogenase similar protein</p> <p>orphan short-chain dehydrogenase / reductase; retinol dehydrogenase similar protein</p> <p>microsomal NAD⁺-dependent retinol dehydrogenase 4</p> <p>11-cis retinol dehydrogenase</p> <p>11-cis retinol dehydrogenase (11-cis RDH)</p> <p>Similar to retinol dehydrogenase 5 (11-cis and 9-cis)</p> <p>epimerase</p> <p>hydroxysteroid epimerase</p> <p>3-hydroxysteroid epimerase</p>
NM_021446 NP_067421.1	F:(C-D)+2.54	
AK007857 XP_125913.2	F:(C-D)+2.54	

AK011472 BAB27642.1	F:(C-IR)+2.53	<p>3-hydroxysteroid epimerase; oxidative 3-alpha-hydroxysteroid-dehydrogenase; 3(alpha->beta)-hydroxysteroid epimerase; retinol dehydrogenase; oxidoreductase; NAD+ -dependent 3 alpha-hydroxysteroid dehydrogenas reductase oxidoreductase splicing factor</p>
AA409743 XP_129542.1	F:(C-D)+2.52	<p>possible role in pre-mrna processing splicing factor p54; arginine-rich 54 kDa nuclear protein arginine-rich nuclear protein Splicing factor arginine/serine-rich 11 (Arginine-rich 54 kDa nuclear protein) (p54) Similar to splicing factor, arginine/serine-rich 11 transgelin</p>
NM_025879 NP_080155.2	F:(C-D)+2.5	<p>transgelin 2; SM22-alpha homolog; TAG2 similar to Homo sapiens mRNA for KIAA0120 gene with GenBank Accession Number D21261.1 hypothetical protein FLJ13611</p>
NM_033354 NP_203505.1	F:(C-D)+2.5	<p>Similar to RIKEN cDNA 2410002O22 gene regucalcin gene promotor region related protein; RGPR-p117</p>
NM_008471 NP_032497.1	F:(C-D)+1.85	<p>FLJ00305 protein cytoskeletal protein keratin keratin related product keratin 14; cytokeratin 14 keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner) similar to keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner) keratin 14, type I, cytoskeletal; (K14) (CK 14) keratin 15 keratin 15; keratin-15, basic; keratin-15, beta; type I cytoskeletal 15; cytokeratin 15; (K15) (CK 15) cytokeratin 15 (AA 1 - 456) keratin 17 Similar to keratin 17 Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1) cytokeratin 17 keratin 19</p>

<p>NM_007494 NP_031520.1</p>	<p>F:(C-D)+1.80</p>	<p>Keratin 19 (AA 1 - 399) Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19) keratin 19; keratin, type I cytoskeletal 19; keratin, type I, 40-kd; cytokeratin 19; 40-kDa keratin intermediate filament precursor gene Unknown (protein for MGC:15366) synthetase</p>
<p>NM_021099 NP_066922.1</p>	<p>F:(C-D)+1.74</p>	<p>argininosuccinate synthetase Argininosuccinate synthase (Citrulline-aspartate ligase) argininosuccinate synthetase (aa 1-412) similar to argininosuccinate synthase (citrulline-aspartate ligase); 84% Similarity to P09034 (NID:g114291) receptor</p>
		<p>transmembrane receptor type 3 transmembrane receptor for MGF (mast cell growth factor) KIT protein protein p145-ckit (AA 1 - 976) mast/stem cell growth factor receptor Mast/stem cell growth factor receptor precursor (SCFR) (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen) v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog precursor protein-tyrosine kinase, receptor type kit precursor human FLT3 receptor tyrosine kinase colony stimulating factor CSF-1 receptor macrophage colony-stimulating factor 1 receptor precursor Macrophage colony stimulating factor I receptor precursor (CSF-1-R) (Fms proto-oncogene) (c-fms) (CD115 antigen) gene c-fms put. c-fms precursor platelet-derived growth factor receptor alpha-platelet-derived growth factor receptor platelet-derived growth factor A receptor platelet-derived growth factor receptor A chain platelet-derived growth factor receptor alpha precursor Alpha platelet-derived growth factor receptor precursor PDGF-R-alpha) (CD140a antigen) platelet-derived growth factor receptor, beta polypeptide platelet-derived growth factor receptor beta precursor Beta platelet-derived growth factor receptor precursor (PDGF-R-beta) (CD140b antigen)</p>

AK012581 BAC25371.1	F:(C-D)+1.60	hypothetical protein SB143
		hypothetical protein MGC10986 AAH04400 Unknown (protein for MGC:10986)
AK007692 BAB25193.1	F:(C-D)+1.62	phospholipid-binding protein
		calcium-dependent phospholipid-binding protein role in the regulation of cellular growth and in signal transduction pathways Annexin A13 (Annexin XIII) (Annexin, intestine-specific) (ISA) annexin A13 isoform b
NM_008655 NP_032681.1	F:(C-IR)+1.64	Growth arrest and DNA-damage-inducible protein
		Growth arrest and DNA-damage-inducible protein GADD45 beta Negative growth-regulatory protein MyD118) (Myeloid differentiation primary response protein MyD118) growth arrest and DNA damage inducible protein beta myeloid differentiation DKFZP566B133 protein; myeloid differentiation primary response; myeloid differentiation primary response gene negative growth-regulatory protein MyD118
AK003571 XP_129443.2	F:(C-IR)+1.62	liprin
		liprin-alpha Liprins interact with members of LAR family of transmembrane protein tyrosine phosphatases interaction may regulate the disassembly of focal adhesion and thus help orchestrate cell-matrix interactions liprin-alpha2 liprin-alpha4 similar to liprin alpha 4 [Rattus norvegicus] PTPRF interacting protein alpha 1 isoform b; LAR-interacting protein 1 LAR-interacting protein 1a LAR-interacting protein 1b LAR-interacting protein LIP1b PPFIA1 protein
AK013489 BAC39584	F:(C-IR)+1.53	transferase
		aminotransferase mitochondrial aminotransferase alanine-glyoxylate aminotransferase alanine-glyoxylate aminotransferase 2 alanine-glyoxylate aminotransferase 2-like 1 Similar to alanine-glyoxylate aminotransferase 2-like 1

		alanine:glyoxylate aminotransferase 2 homolog 1, splice form 1 alanine-glyoxylate aminotransferase 2 precursor; beta-alanine-pyruvate aminotransferase; beta-ALAAT II Alanine-glyoxylate aminotransferase 2, mitochondrial precursor (AGT 2) (Beta-alanine-pyruvate aminotransferase) (Beta-ALAAT II)
NM_008180 NP_032206.1	F:(C-D)+2.60	glutathione synthetase
NM_010344 NP_034474.3	F:(C-D)+2.31	glutathione reductase
		Glutathione reductase, mitochondrial precursor (GR)
		thioredoxin reductase
		thioredoxin reductase II alpha
		thioredoxin reductase II beta
		thioredoxin reductase 1
		thioredoxin reductase 3
AK002661 BAB22268.1	F:(C-D)+2.01	GSTK1 protein
		GSTK1-1
		glutathione transferase kappa 1
NM_010356 NP_034486.2	F:(C-D)+1.73	glutathione transferase
		Glutathione S-transferase A3
		Glutathione S-Transferase A1-1 (E.C.2.5.1.18)
		glutathione S-transferase A2 subunit
		glutathione transferase A5
		glutathione transferase (EC 2.5.1.18) omega-1 chain
		glutathione transferase (EC 2.5.1.18) omega-2 chain
NM_008184 NP_032210.1	F:(C-D)+1.63	glutathione S-transferase
		glutathione transferase M1
		Glutathione S-transferase M3
		Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)
		glutathione transferase M4
		glutathione transferase (EC 2.5.1.18) class mu, GSTM4
		glutathione transferase (EC 2.5.1.18) class mu, GSTM3
NM_008182 NP_032208.1	F:(C-D)+1.51	glutathione transferase
		glutathione S-transferase A1
		Glutathione S-Transferase A1-1
		glutathione S-transferase A2
		Glutathione S-transferase A3
		glutathione S-transferase A4

		glutathione transferase A5
NM_010360		
NP_034490.1	F:(C-D)+1.40	glutathione transferase
		glutathione transferase M1
		Glutathione S-Transferase M1a
		Glutathione S-Transferase M1a-1a
		Glutathione S-Transferase M2
		Glutathione S-Transferase M2-2
		Glutathione S-Transferase M4
		Glutathione S-Transferase M4- 4
		Glutathione S-transferase Mu 5 (GSTM5-5)
J03953		
NP_034489	F:(C-D)+1.40	glutathione transferase M1
		Glutathione S-Transferase M1a-1a
		Glutathione S-Transferase M2
		Glutathione S-Transferase M2-2
		Glutathione S-Transferase M4
		Glutathione S-Transferase M4- 4
		Glutathione S-transferase M5
NM_010363		
NP_034493.1	F:(C-D)+1.20	glutathione transferase zeta 1
NM_008185		
NP_032211.2	F:(C-D)+1.14	Glutathione S-transferase theta 1
		glutathione S-transferase theta 2

Subtable 2B: Unfavorable Mouse Genes/Proteins and Human Protein Classes

NM_009043 NP_033069.1	U:(C-D)30.27 U:(C-IR)13	regenerating protein (reg)
		islet regenerating protein
		Regenerating islet-derived 1 alpha, precursor
		regenerating islet lectin 1-alpha precursor
		lithostathine
		Lithostathine 1 alpha precursor (Pancreatic stone protein) (PSP) (Pancreatic thread protein) (PTP) (Islet of langerhans regenerating protein) (REG) (Regenerating protein 1 alpha) (Islet cells regeneration factor) (ICRF)
		pancreatic stone protein precursor
		regenerating protein I beta
		regenerating islet-derived 1 beta
		regenerating islet-derived 1 beta precursor; lithostathine 1 beta
		Lithostathine 1 beta precursor
		regenerating islet lectin 1-beta precursor
		reg gene homologue
NM_009863 NP_033993.1	U:(C-D)11.89	Cdc7
		CDC7-like 1; Cell division cycle 7, <i>S. Cerevisiae</i> , homolog-like 1
		Cdc7-related kinase
		Cell division cycle 7-related protein kinase (HsCdc7) (huCdc7)
NM_011036 NP_035166.1	U:(C-D)9.09 U:(C-IR)6.83	pancreatitis-associated protein
		pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein
		Pancreatitis-associated protein 1 precursor
		PAP-H
		PAP homologous protein
		similar to pancreatitis-associated protein
		similar to pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein
		Pancreatic beta cell growth factor precursor (Islet neogenesis associated protein)
NM_022328 NP_071723.1	U:(C-D)9 U:(C-IR)5.73	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>); translocated to, 1; Myeloid/lymphoid or mixed-lineage leukemia (trithorax (<i>Drosophila</i>)); myeloid/lymphoid or mixed-lineage leukemia (trithorax (<i>Drosophila</i>) homolog); translocated to, 1

		myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3; Myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila); myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 3
		LTG19
		ENL protein
		AF-9 protein
NM_011259 NP_035389.1	U:(C-D)8.48 U:(C-IR)6.06	pancreatitis-associated protein
		pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein
		Pancreatitis-associated protein 1 precursor
		similar to pancreatitis-associated protein
		similar to pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein
		Pancreatic beta cell growth factor precursor (Islet neogenesis associated protein)
NM_010924 NP_035054.1	U:(C-IR)4.51	methyltransferase
		nicotinamide N-methyltransferase
		Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase) (Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Arrine N-methyltransferase)
		thioester S-methyltransferase-like
D13903 BAA03003.1	U:(C-D)6.19 U:(C-IR)4.37	phosphatase
		protein phosphatase
		protein-tyrosine phosphatase
		protein tyrosine phosphatase delta
		protein tyrosine phosphatase, receptor type
		protein tyrosine phosphatase, receptor type, delta polypeptide
		protein-tyrosine-phosphatase, receptor type delta precursor
		protein tyrosine phosphatase, receptor type, D isoform 2 precursor
		protein tyrosine phosphatase, receptor type, D isoform 3 precursor
		protein tyrosine phosphatase, receptor type, D isoform 4 precursor
		protein tyrosine phosphatase sigma
		protein tyrosine phosphatase, receptor type, sigma isoform 2 precursor
		protein tyrosine phosphatase, receptor type, sigma isoform 3 precursor
		protein tyrosine phosphatase, receptor type, sigma isoform 4 precursor
NM_020494 NP_065240.1	U:(C-D)5.51 U:(IR-D)2.67	helicase
		RNA helicase

		ATP-dependent RNA helicase
		ATP-dependent RNA helicase DDX24 (DEAD-box protein 24)
		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (<i>S.cerevisiae</i> CHL1-like helicase); <i>S.cerevisiae</i> CHL1-like helicase
AK004865	U:(C-D)5.5	synthase
BAB23626.1	U:(IR-D)2.54	
		hydroxymethylglutaryl-Coenzyme A synthase
		Hydroxymethylglutaryl-Coenzyme A synthase, cytoplasmic
		hydroxymethylglutaryl-Coenzyme A synthase, cytosolic, adrenal isoform
		hydroxymethylglutaryl-Coenzyme A synthase, cytosolic, fibroblast isoform
		3-hydroxy-3-methylglutaryl Coenzyme A synthase
		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
		hydroxymethylglutaryl-CoA synthase precursor
		similar to Hydroxymethylglutaryl-Coenzyme A synthase, cytoplasmic
		similar to 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
NM_024406	U:(C-D)5.33	binding protein
NP_077717.1	U:(C-IR)4.36	
		adipocyte lipid-binding protein
		fatty acid binding protein
		Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding protein) (ALBP) (A-FABP)
		fatty acid binding protein 4, adipocyte; A-FABP
NM_011260	U:(C-D)5.05	pancreatitis-associated protein
NP_035390.1	U:(C-IR)3.44	
		pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein
		pancreatitis-associated protein precursor
		Pancreatitis-associated protein 1 precursor
		PAP homologous protein
		similar to pancreatitis-associated protein
		similar to pancreatitis-associated protein precursor; hepatocarcinoma-intestine-pancreas; PAP homologous protein
AK004839	U:(C-IR)3.48	binding protein
XP_129259.1		
		retinol binding protein
		Retinol Binding Protein (Apo Form)
		Retinol Binding Protein (Holo Form)
		precursor RBP
		Plasma retinol-binding protein precursor (PRBP) (RBP) (PRO2222)
		RBP4 gene product

		Similar to retinol binding protein 4, plasma
		E Chain E, The Structure Of Human Retinol Binding Protein With Its Carrier Protein Transthyretin Reveals Interaction With The Carboxy Terminus Of Rbp
		F Chain F, The Structure Of Human Retinol Binding Protein With Its Carrier Protein Transthyretin Reveals Interaction With The Carboxy Terminus Of Rbp
NM_025895 NP_080171.1	U:(C-IR)4.12	tumor angiogenesis marker
		tumor-related protein
		FKSG20
		endothelial-derived gene 1
NM_031162 NP_112439.1	U:(C-D)4.1 U:(C-IR)2.79	receptor
		T-cell receptor
		T-cell receptor zeta chain
		T-cell receptor zeta chain precursor
		T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor T3 zeta chain)
		CD3Z antigen, zeta polypeptide (TtT3 complex)
NM_008745 NP_032771.1	U:(C-IR)3.14	kinase
		protein tyrosine kinase
		protein-tyrosine kinase precursor
		protein tyrosine kinase non catalytic form
		neurotrophic tyrosine kinase receptor
		neurotrophic tyrosine kinase receptor, type 2
		neurotrophin receptor tyrosine kinase type 2 truncated isoform
		brain-derived neurotrophic factor receptor
		brain-derived neurotrophic factor receptor precursor
		brain-derived neurotrophic factor receptor precursor, short splice form
		BDNF/NT-3 growth factors receptor precursor (TrkB tyrosine kinase) (GP145-TrkB) (Trk-B)
		tyrosine kinase receptor p145TRK-B
		neurotrophic tyrosine kinase, receptor, type 3
		neurotrophin receptor trkC precursor
		neurotrophin-3 receptor precursor
		NT-3 growth factor receptor precursor (TrkC tyrosine kinase) (GP145-TrkC) (Trk-C)
NM_010189 NP_034319.1	U:(C-D)3.53 U:(C-IR)3.72	Fc fragment
		Fc receptor
		Fc receptor of IgG
		Fc fragment of IgG, receptor, transporter, alpha

		IgG receptor FcRn large subunit P51 precursor (FcRn) (Neonatal Fc receptor) (IgG Fc fragment receptor transporter, alpha chain)
		FcRn protein
		FcRn alpha chain
AK015750 BAB29956.1	U:(C-IR)3.54	transferase
		sulfotransferase
		Estrogen sulfotransferase (Sulfotransferase, estrogen-preferring) (EST-1)
		thyroid hormone sulfotransferase
		thyroid hormone sulfotransferase B2
		ST1B2
		aryl sulfotransferase
		aryl sulfotransferase, brain iso form
		phenol sulfotransferase
		Phenol-sulfating phenol sulfotransferase 1 (P-PST) (Thermostable phenol sulfotransferase) (Ts-PST) (HAST1/HAST2) (ST1A3)
NM_026189 NP_080465.2	U:(C-D)3.66 U:(C-IR)2.51	KIAA1706 protein
NM_007669 NP_031695.1	U:(C-D)3.6	kinase
		cyclin-dependent kinase
		cyclin-dependent kinase inhibitor
		cyclin-dependent kinase inhibitor isoform
		cyclin-dependent kinase inhibitor 1A (p21, Cip1)
		cyclin-dependent kinase inhibitor 1A; melanoma differentiation associated protein 6 (MDA-6); CDK-interaction protein 1; wild-type p53-activated fragment 1; DNA synthesisinhibitor
		wild type p53 activated fragment-1
		putative DNA synthesis inhibitor
		alternate gene name=WAF1
AK008108 BAB25464.1	U:(C-D)3.54 U:(C-IR)2.98	sulfatase
		glucosamine-6-sulfatase
		similar to glucosamine-6-sulfatases
		extracellular sulfatase SULF-1
		similar to extracellular sulfatase SULF-1; expressed sequence AW121680
		sulfatase SULF1 precursor
		extracellular sulfatase SULF-2
		sulfatase FP
		similar to sulfatase FP
		KIAA1077 protein

		KIAA1247 protein
		dJ1049G16.1.1 (KIAA1247 (similar to glucosamine-6-sulfatases and KIAA1077), isoform 1)
		dJ1049G16.1.2 (KIAA1247 (similar to glucosamine-6-sulfatases and KIAA1077), isoform 2)
NM_010301 NP_034431.1	U:(C-D)2.61	binding protein
		guanine nucleotide binding protein (G protein)
		guanine nucleotide binding protein (G protein), alpha
		guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide-binding protein 14; G-protein alpha subunit 14
		guanine nucleotide binding protein (G protein), alpha 11 (Gq class); guanine nucleotide-binding protein, Gq class, GNA11
		guanine nucleotide binding protein alpha q
		guanine nucleotide binding protein (G protein), q polypeptide
		GTP-binding protein alpha-q
		G alpha-q
		Guanine nucleotide-binding protein G(q), alpha subunit
		GTP-binding regulatory protein Gy alpha chain
		guanine nucleotide-binding regulatory protein
NM_011594 NP_035724.1	U:(C-D)3.51	Tissue inhibitor of metalloproteinases
		Tissue inhibitor of metalloproteinases, Type-2; tissue inhibitor of metalloproteinases-2
		metalloproteinase inhibitor precursor
		tissue inhibitor of metalloproteinase 2 precursor
		Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of metalloproteinases-2) (CSC-21K)
		metalloproteinase-2 inhibitor precursor
		C Chain C, Prommp-2TIMP-2 Complex
		D Chain D, Prommp-2TIMP-2 Complex
		N-Terminal Domain Of Tissue Inhibitor Of Metalloproteinase-2 (N-Timp-2), Nnr, 49 Structures
		Metalloproteinase inhibitor 4 precursor (TIMP-4) (Tissue inhibitor of metalloproteinases-4)
		tissue inhibitor of metalloproteinase 4 precursor
NM_009242 NP_033268.1	U:(C-D)3.49	SPARC (Secreted protein acidic and rich in cysteine); Osteonectin (ON); Basement membrane protein BM-40; extracellular matrix protein BM-40
		osteonectin precursor; SPARC precursor
		SPARC-like protein 1 (High endothelial venule protein) (Hevin) (MAST 9)
		SPARC-like protein 1 precursor; hevin precursor
		Hevin-like protein

NM_023707 NP_076196.1	U:(C-IR)3.46	trypsinogen; trypsin precursor
		mesotrypsin preproprotein; trypsin 4, brain; protease, serine, 4; mesotrypsinogen; trypsin 3; brain trypsinogen; pancreatic trypsinogen III
		trypsinogen IV
		trypsinogen IV a-form
		trypsinogen IV b-form; trypsin IV form b precursor
		protease, serine, 1 preproprotein; cationic trypsinogen; trypsinogen A; trypsinogen I; trypsin 1; trypsin I; trypsin I precursor
		protease, serine, 2 preproprotein; trypsinogen 2; trypsinogen II; anionic trypsinogen; trypsin 2; trypsin II
		trypsinogen C
		trypsinogen E
NM_016850 NP_058546.1	U:(C-D)3.42 U:(C-IR)3.17	interferon regulatory factor
		Interferon regulatory factor 7 (IRF-7)
		interferon regulatory factor 7 isoform b
		interferon regulatory factor 7B
		interferon regulatory factor 7 isoform a
		interferon regulatory factor 7A
		interferon regulatory factor 7 isoform c
		interferon regulatory factor 7H
		putative interferon regulatory factor 7C.2
NM_009799 NP_033929.1	U:(C-D)3.38	anhydrase, carbonic
		carbonic anhydrase I; carbonic dehydratase; Carbonate dehydratase I (CA-I); Carbonic anhydrase B
		Carbonic anhydrase III (Carbonate dehydratase III) (CA-III)
		carbonic anhydrase III, muscle specific
NM_030719 NP_109644.1	U:(C-D)3.36 U:(C-IR)2.93	Unknown (protein for MGC:31979)
NM_010056 NP_034186.1	U:(C-D)3.32	Homeobox protein
		Homeobox protein DLX-5; distal-less homeo box 5
NM_023633 NP_076122.1	U:(C-IR)3.27	nuclear antigen
		myc-induced nuclear antigen
		Mina53
		Mina53 form-2
		myc-induced nuclear antigen, 53 kDa isoform 2; Mina53
NM_013685 NP_038713.1	U:(C-D)3.27	binding protein
		DNA binding protein

NM_009751 NP_033881.1	U:(C-D)3.25	<p>ITF-1 DNA binding protein</p> <p>ITF-2 DNA binding protein</p> <p>transcription factor</p> <p>transcription factor ITF-1</p> <p>transcription factor ITF-2</p> <p>transcription factor 3</p> <p>transcription factor 3; transcription factor E2-alpha; E2A immunoglobulin enhancer-binding factor E12/E47; immunoglobulin transcription factor 1; kappa-E2-binding factor</p> <p>Transcription factor E2-alpha (Immunoglobulin enhancer binding factor E12/E47) (Transcription factor-3) (TCF-3) (Immunoglobulin transcription factor-1) (Transcription factor ITF-1) (Kappa-E2-binding factor)</p> <p>transcription factor 4</p> <p>Transcription factor 4 (Immunoglobulin transcription factor 2) (ITF-2) (SL3-3 enhancer factor 2) (SEF-2)</p> <p>transcription factor 4 isoform b; Transcription factor-4 (immunoglobulin transcription factor-2)</p> <p>transcription factor 12</p> <p>TRANSCRIPTION FACTOR 12 (TRANSCRIPTION FACTOR HTF-4) (E-BOX-BINDING PROTEIN) (DNA-BINDING PROTEIN HTF4)</p> <p>E2A/HLF fusion protein</p> <p>transcription factor HTF4</p> <p>transcription factor E2A</p> <p>e12 protein</p> <p>IMMUNOGLOBULIN ENHANCER BINDING; TRANSCRIPTION FACTOR-3; TCF-3; TRANSCRIPTION FACTOR ITF-1</p> <p>SEF2-1A protein</p> <p>SEF2-1B protein</p> <p>filensin</p>
AK017767 NP_079962.1	U:(C-D)3.23	<p>filensin; lens intermediate filament protein; Lifl-H</p> <p>filensin; cytoskeletal protein, 115 KD</p> <p>Filensin (Beaded filament structural protein 1) (Lens fiber cell beaded-filament structural protein CP 115) (CP11.5) (Lens intermediate filament like-heavy) (LIFL-H)</p> <p>Similar to beaded filament structural protein 1, filensin</p> <p>transcription factor</p> <p>transcription initiation factor</p> <p>RNA polymerase III transcription initiation factor BRFU</p> <p>RNA polymerase III transcription initiation factor BRF2; RNA polymerase III transcription initiation factor BRFU; transcription factor IIB- related factor, TFIIIB50</p> <p>TFIIIB50</p>

NM_008093 NP_032119.1	U:(C-D)3.23	transcription factor GATA transcription factor GATA-4 GATA binding protein 4; GATA-binding protein 4 GATA binding protein 5; transcription factor GATA-5; GATA binding factor-5 bB379O24.1 (novel protein similar to transcription factor GATA-5) Transcription factor GATA-6 (GATA binding factor-6) GATA binding protein 6; GATA-binding protein 6 hGATA-6
NM_010286 NP_034416.1	U:(C-D)3.21 U:(C-IR)3.22	GILZ glucocorticoid-induced GILZ Glucocorticoid-induced leucine zipper protein (Delta sleep-inducing peptide immunoreactor) (DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-like protein) (TSC-22R) TSC-22 related protein TSC-22-like Protein
NM_031388 NP_113565.1	U:(C-D)3.08	protease ubiquitin protease ubiquitin-specific processing protease ubiquitin-specific protease 26 Ubiquitin carboxyl-terminal hydrolase 26 (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) Ubiquitin carboxyl-terminal hydrolase 29 (Ubiquitin thiolesterase 29) (Ubiquitin-specific processing protease 29) (Deubiquitinating enzyme 29) ubiquitin-specific processing protease; likely ortholog of mouse ubiquitin-specific processing protease 29
NM_029796 NP_084072.1	U:(C-D)3.16 U:(C-IR)2.6	glycoprotein leucine-rich alpha-2-glycoprotein Leucine-rich alpha-2-glycoprotein precursor (LRG)
NM_007897 NP_031923.1	U:(C-D)3.15	transcription factor early B-cell transcription factor Similar to early B-cell factor 1 Transcription factor COE1 (OE-1) (O/E-1) (Early B-cell factor) Transcription factor COE2 (Early B-cell factor 2) (EBF-2) Transcription factor COE3 (Early B-cell factor 3) (EBF-3) (Olf-1/EBF-like 2) (OE-2) (O/E-2) similar to Transcription factor COE3 (Early B-cell factor 3) (EBF-3) (Olf-1/EBF-like 2) (OE-2) (O/E-2)

NM_007693 NP_031719.1	U:(C-D)3.1	<p>Transcription factor COE4 (Early B-cell factor 4) (EBF-4) (OLF-1/EBF-like 4) (OE-4) (O/E-4)</p> <p>dJ860F19.1.1 (KIAA1442 (similar to olfactory neuronal transcription factors (COE1, COE2, COE3, EBF3, OLF1))) (isoform 1))</p> <p>dJ860F19.1.2 (novel protein similar to olfactory neuronal transcription factors (COE1, COE2, COE3, EBF3, OLF1) (isoform 2))</p> <p>similar to dJ860F19.1.2 (novel protein similar to olfactory neuronal transcription factors (COE1, COE2, COE3, EBF3, OLF1) (isoform 2))</p> <p>chromogranin A</p>
NM_013569 NP_038597.1	U:(C-D)3.09	<p>chromogranin A precursor</p> <p>Similar to chromogranin A (parathyroid secretory protein 1)</p> <p>chromogranin A; parathyroid secretory protein 1</p> <p>Chromogranin A precursor (CGA) (Pituitary secretory protein I) (SP-I) [Contains: Vasostatin I; Vasostatin II; EA-92; ES-43; Pancreastatin; SS-18; WA-8; WE-14; LF-19; AL-11; GV-19; GR-44; ER-37]</p> <p>channel</p> <p>potassium channel</p> <p>potassium channel subunit</p> <p>potassium channel 1b protein</p> <p>Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go related gene potassium channel 1) (H-ERG) (Erg1) (Ether-a-go-go related protein 1) (Eag related protein 1) (eag homolog)</p> <p>Similar to potassium voltage-gated channel, subfamily H (eag-related), member 2</p> <p>voltage-gated potassium channel, subfamily H, member 2 isoform a; potassium voltage-gated channel, subfamily H, member 2; ether-a-go-go-related potassium channel protein; human eag-related gene</p> <p>voltage-gated potassium channel, subfamily H, member 2 isoform b; potassium voltage-gated channel, subfamily H, member 2; ether-a-go-go-related potassium channel protein; human eag-related gene</p> <p>voltage-gated potassium channel, subfamily H, member 2 isoform c; potassium voltage-gated channel, subfamily H, member 2; ether-a-go-go-related potassium channel protein; human eag-related gene</p> <p>Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go related gene potassium channel 3) (HERG-3) (Ether-a-go-go related protein 3) (Eag related protein 3)</p> <p>Similar to potassium voltage-gated channel, subfamily H (eag-related), member 7</p> <p>potassium voltage-gated channel, subfamily H, member 7 isoform 1; potassium channel subunit HERG-3; ether-a-go-go related gene potassium channel 3; eag related protein 3</p> <p>Potassium voltage-gated channel, subfamily H, member 7 isoform 2; potassium channel subunit HERG-3; ether-a-go-go related gene potassium channel 3; eag related protein 3</p> <p>ether-a-go-go-related K⁺ channel protein</p> <p>ether-a-go-go related potassium channel</p>

NM_011248 NP_035378.1	U:(C-IR)3.08	ether-a-go-go-related protein a gene responsible for familial long QT syndrome (LQT2) HERG-USO. receptor roundabout 1 roundabout 1 isoform a; roundabout 1; axon guidance receptor roundabout 1 isoform b; roundabout 1; axon guidance receptor roundabout 2 hemicentin fibulin-6
AK016257 CAC84526.1	U:(C-D)3.03 U:(C-IR)2.74	transferase ribosyltransferase ADP ribosyltransferase mono-ADP-ribosyltransferase ADP-ribosyltransferase 3 Ecto-ADP-ribosyltransferase 3 precursor (NAD(P)(+)-arginine ADP-ribosyltransferase 3) (Mono(ADP-ribosyl)transferase 3)
AF064749 AAC23667.1	U:(C-D)3.02	collagen collagen alpha collagen alpha 3 collagen alpha 3 (VI) Collagen alpha 3(VI) chain precursor Similar to collagen, type VI, alpha 3 alpha 3 type VI collagen isoform 1 precursor; collagen VI, alpha-3 polypeptide alpha 3 type VI collagen isoform 2 precursor; collagen VI, alpha-3 polypeptide alpha 3 type VI collagen isoform 3 precursor; collagen VI, alpha-3 polypeptide alpha 3 type VI collagen isoform 4 precursor; collagen VI, alpha-3 polypeptide alpha 3 type VI collagen isoform 5 precursor; collagen VI, alpha-3 polypeptide
NM_025725 NP_080001.1	U:(C-IR)3.01	hypothetical protein FLJ90575
NM_007643 NP_031669.1	U:(C-IR)2.65	unnamed protein product receptor CD36 CD36 antigen cell adhesion receptor CD36 CD36 antigen (collagen type I receptor, thrombospondin receptor)

NM_020564
NP_065589.1

U:(C-D)3

Similar to CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1
 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)
 CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36 antigen (collagen type I); cluster determinant 36; fatty acid translocase; scavenger receptor class B, member 3
 scavenger receptor class B, member 1; CD36 antigen-like 1; scavenger receptor class B type 1; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1
 scavenger receptor class B, member 2; CD36 antigen (collagen type I receptor, thrombospondin receptor) -; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)
 lysosomal membrane protein
 lysosomal integral membrane protein II
 Lysosome membrane protein II (LIMP II) (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2)
 85kDa lysosomal sialoglycoprotein
 glycoprotein GPIIb/GPIV
 Platelet glycoprotein IV (GPIV) (GPIIb) (CD36 antigen) (PAS IV) (PAS-4 protein)
 CLA-1
 membrane glycoprotein CLA-1 protein long form precursor
 transferase
 sulfotransferase
 sulfotransferase family, cytosolic, 1A, phenol-prefering, member 2; thermostable phenol sulfotransferase; phenolic-metabolizing (P) form of PST; arylamine sulfotransferase; aryl sulfotransferase; phenol-prefering phenol sulfotransferase2; phenol-sulfating phenol sulfotransferase 2
 sulfotransferase family, cytosolic, 2B, member 1; sulfotransferase family 2B, member 1
 hydroxysteroid sulfotransferase
 hydroxysteroid sulfotransferase SULT2B1a
 hydroxysteroid sulfotransferase SULT2B1b
 alcohol sulfotransferase
 Alcohol sulfotransferase (Hydroxysteroid Sulfotransferase) (HST) (Dehydroepiandrosterone sulfotransferase) (DHEA-ST) (ST2) (ST2A3)
 alcohol sulfotransferase; hydroxysteroid sulfotransferase
 alcohol/hydroxysteroid sulfotransferase; hSTa
 dehydroepiandrosterone sulfotransferase
 aryl sulfotransferase
 phenol sulfotransferase
 ES18

NM_022882 NP_075020.1	U:(C-D)2.97	<p>lipin</p> <p>lipin 1</p> <p>Similar to lipin 1</p> <p>lipin 2</p> <p>Lipin 3</p> <p>[Segment 2 of 3] Lipin 3 (Lipin 3-like)</p> <p>[Segment 3 of 3] Lipin 3 (Lipin 3-like)</p>
NM_010730 NP_034860.1	U:(C-D)2.97	<p>binding protein</p> <p>Ca(2+)- and phospholipid-binding protein</p> <p>annexin</p> <p>annexin I</p> <p>annexin I; annexin I (lipocortin I); lipocortin I</p> <p>Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35) (Phospholipase A2 inhibitory protein)</p> <p>annexin II</p> <p>annexin A1</p> <p>similar to annexin A1</p> <p>annexin A2</p> <p>annexin A2; annexin II; annexin II (lipocortin II); calpactin I, heavy polypeptide (p36); lipocortin II; Annexin II (lipocortin I); annexin II (lipocortin II); calpactin I, heavy polypeptide)</p> <p>bA255A11.8 (novel protein similar to annexin A2 (ANXA2) (lipocortin II, calpactin I heavy chain, chromobindin 8, PAP-IV))</p> <p>annexin III</p> <p>Annexin III (Lipocortin III) (Placental anticoagulant protein III) (PAP-III) (35-alpha calcimedlin) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase)</p> <p>annexin A3</p> <p>annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III, 1,2-cyclic-inositol-phosphate phosphodiesterase, placental anticoagulant protein III, calcimedlin 35-alpha); calcimedlin 35-alpha</p> <p>annexin VII isoform 1; annexin VII (synexin); synexin</p> <p>annexin A7</p> <p>Annexin A7 (Annexin VII) (Synexin)</p> <p>synexin</p> <p>annexin XI</p> <p>annexin A11</p> <p>annexin A11; annexin XI; autoantigen, 56-kD; calyculin-associated annexin 50</p> <p>Annexin A11 (Annexin XI) (Calyculin-associated annexin 50) (CAP-50) (56 kDa autoantigen)</p> <p>lipocortin</p>

		lipocortin (AA 1-346) lipocortin II lipocortin-III Calpactin
NM_009616 NP_033746.1	U:(C-IR)2.95	<p>ANX2_HUMAN Annexin II (Lipocortin II) (Calpactin I heavy chain) (Chromobindin 8) (P36) (Protein I) (Placental anticoagulant protein IV) (PAP-IV)</p> <p>Annexin Family Mol_id: 1; Molecule: Annexin Iii; Chain: Null; Engineered: Yes; Other_details: Human Recombinant</p> <p>Annexin Iii Co-Crystallized With Inositol-2-Phosphate</p> <p>1,2-cyclic-inositol-phosphate phosphodiesterase</p> <p>a disintegrin and metalloprotease domain</p> <p>a disintegrin and metalloprotease domain 12</p> <p>ADAM 12 precursor (A disintegrin and metalloproteinase domain 12) (Meltrin alpha)</p> <p>a disintegrin and metalloprotease domain 12 isoform 1 preproprotein; A disintegrin and metalloproteinase domain 12 (Meltrin-alpha, mouse, homolog of); meltrin alpha</p> <p>a disintegrin and metalloprotease domain 12 isoform 2 preproprotein; A disintegrin and metalloproteinase domain 12 (Meltrin-alpha, mouse, homolog of); meltrin alpha</p> <p>disintegrin and metalloproteinase ADAM19</p> <p>disintegrin and metalloproteinase domain 19</p> <p>a disintegrin and metalloproteinase domain 19 isoform 2 preproprotein; meltrin beta</p> <p>a disintegrin and metalloproteinase domain 19 isoform 1 preproprotein; meltrin beta</p> <p>ADAM 19 precursor (A disintegrin and metalloproteinase domain 19) (Meltrin beta) (Metalloprotease and disintegrin dentritic antigen marker) (MADDAM)</p> <p>metalloprotease-disintegrin meltrin beta</p> <p>meltrin-L precursor</p> <p>meltrin-beta/ADAM 19 homologue</p> <p>meltrin-S</p>
NM_026294 NP_080570.1	U:(C-D)2.94	<p>binding protein</p> <p>GTP-binding protein</p> <p>GTP-binding protein rhoA</p> <p>small GTP binding protein RhoA</p> <p>Transforming protein RhoA (H12)</p> <p>ras homolog gene family, member A</p> <p>ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho12; RhoA; Ras homolog gene family, member A (oncogene RHO H12)</p> <p>Human Rhoa Complexed With Gtp Analogue</p>

		<p>rhoB [Homo sapiens] GTP-binding protein rhoB - human small GTP binding protein RhoB Transforming protein RhoB (H6) ras homolog gene family, member B; Aplysia RAS-related homolog 6 (oncogene RHO H6); Aplysia ras-related homolog 6; RhoB; RAS homolog gene family, member B (oncogene RHO H6) GTP-binding protein rhoC rhoC coding region (AA 1-193) ORF (AA 1-193) small GTP binding protein RhoC Transforming protein RhoC (H9) ras homolog gene family, member C ras homolog gene family, member C; Aplysia RAS-related homolog 9 (oncogene RHO H9); Aplysia ras-related homolog 9; RhoC; RAS homolog gene family, member C (oncogene RHO H9) GTPase multidrug resistance protein B Chain B, RhoRHOGAPGDP(DOT)ALF4 COMPLEX</p>
<p>NM_016780 NP_058060.1</p>	<p>U:(C-D)2.92</p>	<p>glycoprotein platelet glycoprotein platelet glycoprotein III glycoprotein IIIa, platelet glycoprotein IIIa platelet glycoprotein IIIa precursor, glycoprotein IIIa precursor platelet glycoprotein IIIa-II platelet membrane glycoprotein IIIa beta subunit platelet glycoprotein IIIa beta chain precursor (version 1) platelet glycoprotein IIIa beta chain (version 2) Integrin Integrin beta Integrin beta-3 precursor (Platelet membrane glycoprotein IIIa) (GPIIIa) (CD61 antigen) integrin beta-5 subunit</p>
<p>NM_008075 NP_032101.1</p>	<p>U:(C-D)2.89</p>	<p>receptor gamma-amino butyric acid (GABA) gamma-aminobutyric acid (GABA) receptor, rho 1; gamma-aminobutyric acid (GABA) A receptor, rho-1 Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor) gamma-aminobutyric acid receptor A rho-1 chain precursor</p>

		<p>dJ131H7.1 (gamma-aminobutyric acid (GABA) receptor rho 2)</p> <p>GABAA receptor beta 2 subunit</p> <p>gamma-aminobutyric acid A receptor beta 2 subunit; (GABA)A receptor beta 2 subunit</p> <p>gamma-aminobutyric acid (GABA) receptor, rho 2 precursor</p> <p>Gamma-aminobutyric-acid receptor rho-2 subunit precursor (GABA(A) receptor)</p> <p>gamma-aminobutyric acid receptor rho-2 chain precursor</p> <p>Gamma-aminobutyric-acid receptor beta-2 subunit precursor (GABA(A) receptor)</p> <p>gamma-aminobutyric acid (GABA) A receptor, beta 2 isoform 2</p> <p>gamma-aminobutyric acid (GABA) A receptor, beta 3</p> <p>Gamma-aminobutyric-acid receptor beta-3 subunit precursor (GABA(A) receptor)</p> <p>similar to Gamma-aminobutyric-acid receptor rho-3 subunit precursor (GABA(A) receptor)</p> <p>gamma-aminobutyric acid (GABA) A receptor, beta 3 isoform 1 precursor</p> <p>gamma-aminobutyric acid (GABA) A receptor, beta 3 isoform 2 precursor</p> <p>gamma-aminobutyric acid A receptor beta 3 chain splice form 1</p> <p>GABA-alpha receptor beta-3 subunit</p> <p>gamma-aminobutyric acid (GABA) A receptor, delta</p> <p>GABA-A receptor delta subunit</p> <p>Gamma-aminobutyric-acid receptor delta subunit precursor (GABA(A) receptor)</p>
NM_010776 NP_034906.1	U:(C-D)2.76 U:(C-IR)2.88	<p>binding protein</p> <p>mannose binding protein</p> <p>mannose binding lectin</p> <p>mannose-binding lectin precursor</p> <p>mannan-binding lectin MBL precursor</p> <p>soluble mannose-binding lectin precursor; mannose-binding lectin; mannose binding protein; Mannose-binding lectin 2, soluble (opsonic defect)</p> <p>Mannose-binding protein C precursor (MBP-C) (MBP1) (Mannan-binding protein) (Mannose-binding lectin)</p>
NM_009841 NP_033971.1	U:(C-D)2.87	<p>CD14 antigen</p> <p>monocyte antigen CD14</p> <p>monocyte antigen CD14 precursor</p> <p>monocyte surface glycoprotein CD14 precursor</p> <p>cd14 protein precursor</p> <p>CD14 antigen precursor</p> <p>Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein)</p>

AK002477 BAB22130.1	U:(C-D)2.86 U:(C-IR)2.73	leucine-rich preprotein (AA -19 to 356) lipin
		proteolipin plasmolipin similar to plasmolipin
NM_026104 NP_080380.1	U:(C-D)2.84 U:(C-IR)2.54	hypothetical protein MGC35118
		Similar to RIKEN cDNA 1700095F04 gene unnamed protein product
NM_008737 NP_032763.1	U:(C-D)2.83	receptor
		endothelial growth factor receptor vascular endothelial growth factor receptor novel vascular endothelial growth factor receptor neuropilin neuropilin 1 Similar to neuropilin 1 Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor) soluble neuropilin-1 neuropilin-1 soluble isoform 11 neuropilin 2 Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2) neuropilin-2(a0) neuropilin-2(a17) neuropilin-2a(22) vascular endothelial cell growth factor 165 receptor/neuropilin vascular endothelial cell growth factor 165 receptor 2
U28789 AAB49620.1	U:(C-D)2.82 U:(C-IR)2.79	binding protein
		RB protein binding protein retinoblastoma-binding protein 6 retinoblastoma binding protein RBQ-1 proliferation potential-related protein hypothetical protein DKFZp761B2423.1
NM_010287 NP_034417.1	U:(C-IR)2.82	receptor
		glucocorticoid induced receptor G protein-coupled receptor 72; G-protein coupled receptor GPR72; G-protein coupled receptor 72 Probable G protein-coupled receptor GPR72 precursor

NM_016759 NP_058039.1	U:(C-D)2.81	orphan G-protein coupled receptor GPR72 binding protein
AK004851 NP_598514.1	U:(IR-D)2.81	Rap2 binding protein Rap2 interacting protein 8 Rap2 binding protein 9 adaptor protein
NM_023061 NP_075548.1	U:(C-D)2.81 U:(C-IR)2.52	Mitogen-inducible gene 6 protein (Mig-6) Mig-6=mitogen-inducible gene mig-6 product [human, WI-38 cells, Peptide, 462 aa] Gene 33/Mig-6 glycoprotein
AF263458 AAF76887.1	U:(C-D)2.8	melanoma associated glycoprotein MUC18 glycoprotein Cell surface glycoprotein MUC18 precursor (Melanoma-associated antigen MUC18) (Melanoma-associated antigen A32) (S-endo1 endothelial-associated antigen) (CD146 antigen) (Melanoma adhesion molecule) melanoma cell adhesion molecule; melanoma adhesion molecule cell surface glycoprotein P1H12 precursor Lutheran blood group glycoprotein Lutheran blood group glycoprotein precursor Lutheran blood group (Anberger b antigen included); B-cell adhesion molecule; Lutheran blood group; Auberger blood group Lutheran blood group glycoprotein precursor (B-CAM cell surface glycoprotein) (Auberger B antigen) (F8/G253 antigen) B-CAM B-CAM protein placenta-specific 8 BM-004 C15 protein Similar to hypothetical protein
NM_009250 NP_033276.1	U:(C-IR)2.8	protease inhibitor serine protease inhibitor extracellular serine protease inhibitor neuroserpin Neuroserpin precursor (Protease inhibitor 12) protease inhibitor 14; pancpin serpin-like protein

		<p>Serpin I2 precursor (Myoepithelium-derived serine protease inhibitor) (Pancpin) (Protease inhibitor 14) (TSA2004) TSA2004</p> <p>glia-derived nexin precursor</p> <p>glia-derived nexin I precursor, splice form beta</p> <p>protease nexin I</p> <p>Glia derived nexin precursor (GDN) (Protease nexin I) (PN-1) (Protease inhibitor 7)</p> <p>prebeta-migrating plasminogen activator inhibitor</p> <p>Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial plasminogen activator inhibitor) (PAI)</p> <p>precursor polypeptide</p> <p>plasminogen activator-1</p> <p>plasminogen activator inhibitor</p> <p>plasminogen activator inhibitor-1</p> <p>plasminogen activator inhibitor-1; plasminogen activator inhibitor, type I</p> <p>plasminogen activator inhibitor type 1, member 2; protease inhibitor 7 (protease nexin I); glial-derived nexin 1; glial-derived neurite promoting factor</p> <p>plasminogen activator inhibitor-1 precursor</p> <p>serine-cysteine proteinase inhibitor clade E member 1</p> <p>Serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1</p> <p>Serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2</p> <p>serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1; protease inhibitor 12 (neuroserpin)</p> <p>serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1</p> <p>serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 2</p>
<p>NM_009706</p> <p>NP_033836.1</p>	<p>U:(C-D)2.72</p> <p>U:(C-IR)2.8</p>	<p>GTPase activating protein</p> <p>Rho GTPase activating protein</p> <p>Rho GTPase activating protein 5</p> <p>similar to Rho GTPase activating protein 5 [Mus musculus]</p> <p>Rho GAP p190-A</p> <p>Rho GTPase activating protein 5; RhoGAP5; p190-B</p> <p>Rho GTPase activating protein 5 (p190-B) [imported]</p> <p>p190-B</p> <p>glucocorticoid receptor DNA binding factor 1 isoform a</p> <p>glucocorticoid receptor repression factor 1</p> <p>DNA-binding protein GRF-1</p> <p>transporter</p>
<p>NM_021301</p> <p>NP_067276.1</p>	<p>U:(C-IR)2.8</p>	

		peptide transporter H ⁺ /peptide cotransporter intestinal H ⁺ /peptide cotransporter Caco-2 oligopeptide transporter solute carrier family 15 (oligopeptide transporter), member 1; peptide transporter HPEPT1 bA551M18.1.1 (solute carrier family 15 (oligopeptide transporter) member 1) solute carrier family 15 (H ⁺ /peptide transporter), member 2 similar to solute carrier family 15 (H ⁺ /peptide transporter), member 2 Oligopeptide transporter, small intestine isoform (Peptide transporter 1) (Intestinal H ⁺ /peptide cotransporter) (Solute carrier family 15, member 1) Oligopeptide transporter, kidney isoform (Peptide transporter 2) (Kidney H ⁺ /peptide cotransporter) (Solute carrier family 15, member 2) peptide transporter peptide transport protein hPEPT1 PEPT 2 pH-sensing regulatory factor pH-sensing regulatory factor of peptide transporter ribosomal protein
AK008098 BAB25458.1	U:(C-D)2.8	ribosomal protein L4 60S ribosomal protein L4 (L1) ribosomal protein L4; 60S ribosomal protein L4; homologue of Xenopus ribosomal protein L1 Similar to ribosomal protein L4 similar to ribosomal protein L4; 60S ribosomal protein L4; homologue of Xenopus ribosomal protein L1
NM_030257 NP_084533.1	U:(C-D)2.79	similar to cDNA sequence BC003322; hypothetical protein, MGC:7041 [Mus musculus] hypothetical protein DKFZp727I021.1 hypothetical protein
AK010201 BAB26764.1	U:(C-D)2.79 U:(C-IR)2.6	binding protein zinc binding protein yippee protein Yippee homolog (CGI-127) Yippee protein [imported] CGI-127 protein
NM_008344 NP_032370.1	U:(C-D)2.77	binding protein growth factor binding protein insulin-like growth factor binding protein

NM_053254 NP_444484.1	U:(C-D)2.77	<p>IGF-BP 4</p> <p>insulin-like growth factor binding protein 6</p> <p>Insulin-like growth factor binding protein 6 precursor (IGFBP-6) (IBP-6) (IGF-binding protein 6)</p> <p>hypothetical protein FLJ14009</p>
NM_013750 NP_038778.1	U:(C-IR)2.54	<p>R26610_1</p> <p>pleckstrin homology-like domain</p> <p>pleckstrin homology-like domain, family A, member 3; pleckstrin homology-like domain, family A, member 2</p> <p>Similar to pleckstrin homology-like domain, family A, member 3</p> <p>TDAG51/Ipl homologue 1</p>
NM_011254 NP_035384.1	U:(C-IR)2.75	<p>binding protein</p> <p>retinol-binding protein</p> <p>retinol-binding protein, cellular</p> <p>retinol binding protein 1, cellular; retinol-binding protein 1, cellular</p> <p>Retinol-binding protein I, cellular (Cellular retinol-binding protein) (CRBP)</p>
NM_019576 NP_062522.1	U:(C-IR)2.74	<p>TMTSP for transmembrane molecule with thrombospondin module</p>
NM_026002 NP_080278.2	U:(C-IR)2.74	<p>LYRIC</p>
NM_009368 NP_033394.1	U:(C-D)2.72	<p>LYRIC protein</p> <p>growth factor</p> <p>transforming growth factor</p> <p>G-Tsf precursor</p> <p>TGF-beta precursor</p> <p>transforming growth factor beta</p> <p>Similar to transforming growth factor, beta 1</p> <p>transforming growth factor, beta 1 (Camurati-Engelmann disease); transforming growth factor, beta 1; diaphyseal dysplasia1, progressive (Camurati-Engelmann disease)</p> <p>Transforming growth factor beta 1 precursor (TGF-beta 1)</p> <p>Transforming Growth Factor Type Beta 2 (Tgf-B2)</p> <p>transforming growth factor-beta-2 precursor</p> <p>Transforming growth factor beta 2 precursor (TGF-beta 2) (Glioblastoma-derived T-cell suppressor factor) (G-TSF) (BSC-1 cell growth inhibitor) (Polygerin) (Cetermin)</p> <p>transforming growth factor beta-2 precursor, short form</p> <p>transforming growth factor beta-2 precursor, long form</p> <p>transforming growth factor, beta 3</p>

		<p>TGF-beta 3 (AA 1-412)</p> <p>Similar to transforming growth factor, beta 3</p> <p>Transforming growth factor beta 3 precursor (TGF-beta 3)</p> <p>Human Transforming Growth Factor Beta 3, Crystallized From Peg 4000</p> <p>Human Transforming Growth Factor-Beta 3, Crystallized From Dioxane</p> <p>Unknown (protein for MGC:22008)</p>
NM_030256 NP_084532.1	U:(IR-D)2.72	similar to cDNA sequence BC003321; hypothetical protein, MGC:7014 [Mus musculus]
NM_007617 NP_031643.1	U:(IR-D)2.71	<p>membrane protein</p> <p>caveolin</p> <p>Caveolin-1</p> <p>caveolin 1; caveolin 1, caveolae protein, 22kD; caveolae protein, 22-kD; caveolin 1 caveolae protein, 22kD; caveolin 1, alpha isoform; caveolin 1, beta isoform</p> <p>Similar to caveolin 1, caveolae protein, 22kD</p> <p>caveolin 3</p> <p>caveolin 3; M-caveolin; caveolin-3</p>
NM_008107 NP_032133.1	U:(C-D)2.71	<p>GDF-1</p> <p>GDF-1 embryonic growth factor</p> <p>growth differentiation factor 1</p> <p>Embryonic growth/differentiation factor 1 precursor (GDF-1)</p>
NM_025684 NP_079960.1	U:(C-D)2.7	similar to RIKEN cDNA 5730521E12 [Mus musculus]
NM_009305 NP_033331.1	U:(C-D)2.7	<p>synaptophysin</p> <p>synaptophysin; major synaptic vesicle protein P38</p> <p>synaptophysin-like protein; pantophysin</p> <p>Similar to synaptorin</p> <p>Similar to synaptophysin-like protein</p> <p>pantophysin</p> <p>h-Sp</p>
NM_010434 NP_034564.1	U:(C-D)2.7	<p>protein kinase</p> <p>PKY protein kinase</p> <p>homeodomain-interacting protein kinase-1</p> <p>Similar to homeodomain interacting protein kinase 1</p> <p>homeodomain-interacting protein kinase 1; homeodomain interacting protein kinase 1-like protein; nuclear body associated kinase 2b</p> <p>protein kinase HIPK2</p> <p>homeodomain interacting protein kinase 2</p>

NM_011775 NP_035905.1	U:(C-D)2.68	<p>dJ8L15.1 (homeodomain-interacting protein kinase 3)</p> <p>Fas-interacting serine/threonine kinase 3</p> <p>receptor</p> <p>sperm receptor</p> <p>zona pellucida ZP2</p> <p>zona pellucida ZP2 glycoprotein</p> <p>zona pellucida glycoprotein 2 preproprotein; zona pellucida sperm-binding protein 2 precursor; zona pellucida protein A</p> <p>Zona pellucida sperm-binding protein 2 precursor (Zona pellucida glycoprotein ZP2) (Zona pellucida protein A)</p> <p>sperm-binding glycoprotein ZP2 precursor</p>
AF262986 AAK58180.1	U:(C-D)2.68	phosphatase
	U:(C-IR)2.58	<p>protein phosphatase</p> <p>FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a</p> <p>FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b</p> <p>FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1c</p> <p>FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2</p> <p>myotubularin</p> <p>myotubularin-related protein 2</p> <p>myotubularin-related protein 3 isoform a; FYVE (Fab1 YGLO23 Vsp27 EEA1 domain) dual-specificity protein phosphatase; zinc finger, FYVE domain containing 10</p> <p>myotubularin-related protein 3 isoform b; FYVE (Fab1 YGLO23 Vsp27 EEA1 domain) dual-specificity protein phosphatase; zinc finger, FYVE domain containing 10</p> <p>myotubularin-related protein 3 isoform c; FYVE (Fab1 YGLO23 Vsp27 EEA1 domain) dual-specificity protein phosphatase; zinc finger, FYVE domain containing 10</p> <p>myotubularin related protein 4</p> <p>myotubularin related protein 4; zinc finger, FYVE domain containing 11</p>
NM_033374 NP_203538.1	U:(C-D)2.59	dedicator of cyto-kinesis
	U:(C-IR)2.68	<p>dedicator of cyto-kinesis 1</p> <p>Similar to dedicator of cyto-kinesis 1</p> <p>similar to dedicator of cyto-kinesis 2 [Mus musculus]</p> <p>DOCK180 protein</p> <p>similar to a human major CRK-binding protein DOCK180.</p>
NM_018733 NP_061203.1	U:(C-D)2.68	<p>channel</p> <p>sodium channel</p>

		<p>voltage-gated sodium channel</p> <p>voltage-gated sodium channel type I</p> <p>Voltage-gated sodium channel alpha 1 subunit</p> <p>voltage-gated sodium channel alpha subunit SCN1A</p> <p>voltage-gated sodium channel type II alpha subunit</p> <p>Sodium channel protein, brain II alpha subunit</p> <p>sodium channel, voltage-gated, type II, alpha 2; sodium channel, voltage-gated, type II, alpha 2 polypeptide</p> <p>Sodium channel protein, brain III alpha subunit (Voltage-gated sodium channel subtype III)</p> <p>sodium channel alpha chain HBA</p>
<p>NM_016758</p> <p>NP_058038.1</p>	<p>U:(C-IR)2.67</p>	<p>regulator of G protein signaling</p> <p>regulator of G protein signaling 12</p> <p>Regulator of G-protein signaling 12 (RGS12)</p> <p>Regulator of G-protein signaling 14</p> <p>regulator of G-protein signalling 14; regulation of G protein signaling 14</p> <p>regulator of G protein signalling RGS14</p> <p>Similar to regulator of G-protein signaling 14</p> <p>RGS12TS-S isoform</p> <p>regulator of G protein signaling RGS14-variant</p> <p>regulator of G protein signalling 14 short variant</p>
<p>NM_018782</p> <p>NP_061252.1</p>	<p>U:(IR-D)2.67</p>	<p>receptor</p> <p>calcitonin receptor</p> <p>Calcitonin receptor precursor (CT-R)</p> <p>calcitonin receptor isoform</p> <p>calcitonin receptor-like protein</p> <p>truncated isomer of calcitonin receptor</p> <p>Calcitonin Receptor, alternatively spliced form</p> <p>Calcitonin gene-related peptide type 1 receptor precursor (CGRP type 1 receptor)</p>
<p>NM_009776</p> <p>NP_033906.1</p>	<p>U:(C-D)2.67</p>	<p>C1 esterase inhibitor</p> <p>C1-inhibitor</p> <p>C1 inhibitor (AA 155-478) (1 is 2nd base in codon)</p> <p>plasma protease (C1) inhibitor precursor</p> <p>complement C1 inhibitor precursor</p> <p>serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1</p> <p>complement component 1 inhibitor precursor; serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1</p>

NM_010343 NP_034473.1	U:(C-D)2.67	<p>Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh)</p> <p>peroxidase</p> <p>glutathione peroxidase</p> <p>extracellular glutathione peroxidase</p> <p>Epididymal secretory glutathione peroxidase precursor(Epididymis-specific glutathione peroxidase-like protein) (BGLP)</p> <p>similar to EPIDIDYMAL SECRETORY GLUTATHIONE PEROXIDASE PRECURSOR (EPIDIDYMIS-SPECIFIC GLUTATHIONE PEROXIDASE-LIKE PROTEIN) (BGLP)</p> <p>plasma glutathione peroxidase</p> <p>plasma glutathione peroxidase 3 precursor</p> <p>Plasma glutathione peroxidase precursor (GSHPx-F) (Extracellular glutathione peroxidase) (GPx-F)</p> <p>glutathione peroxidase type 5 (GPX5)</p> <p>dJ1186N24.2 (glutathione peroxidase 5 (epididymal androgen-related protein))</p> <p>glutathione peroxidase 5 precursor isoform 1; epididymal androgen-related protein</p> <p>lutathione peroxidase 3, precursor</p>
AK009460 BAB26301.1	U:(C-D)2.66	<p>cyclophilin</p> <p>cyclophilin-like protein</p> <p>cyclophilin-like protein CyP-60</p> <p>cyclophilin:ISOTYPE=CyP-60</p> <p>peptidylprolyl isomerase (cyclophilin)-like 2</p> <p>Peptidyl-prolyl cis-trans isomerase like 2 (PPIase) (Rotamase) (Cyclophilin-60)</p> <p>(Cyclophilin-like protein Cyp-60)</p> <p>Similar to peptidylprolyl isomerase (cyclophilin)-like 2</p> <p>peptidylprolyl isomerase-like 2 isoform a; cyclophilin-like protein CyP-60;</p> <p>peptidylprolyl cis-trans isomerase; cyclophilin, 60kDa</p> <p>peptidylprolyl isomerase-like 2 isoform b; cyclophilin-like protein CyP-60;</p> <p>peptidylprolyl cis-trans isomerase; cyclophilin, 60kDa</p>
NM_025806 NP_080082.1	U:(C-IR)2.65	<p>hypothetical protein FLJ22662</p> <p>unnamed protein product</p> <p>hypothetical protein FLJ22662</p> <p>hypothetical protein LOC196463</p> <p>similar to RIKEN cDNA 1300012G16</p>
AK008273 Q61599	U:(C-D)2.65	<p>GDP dissociation inhibitor</p> <p>rho GDP dissociation inhibitor (GDI)</p> <p>Rho-GDP-dissociation inhibitor Ly-GDI</p> <p>rho protein GDP-dissociation inhibitor 1 (IEF 8118)</p>

NM_008476 NP_032502.1	U:(C-D)2.5	<p>Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)</p> <p>Rho GDP dissociation inhibitor (GDI) alpha</p> <p>Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI)</p> <p>Rho GDP dissociation inhibitor (GDI) beta</p> <p>Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI</p> <p>keratin</p>
		<p>keratin type II</p> <p>KKeratin, type II cytoskeletal 5 (Cytokeratin 5) (K5) (CK 5) (58 kDa cyto keratin)</p> <p>keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)</p> <p>Similar to keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)</p> <p>keratin 5; Keratin-5; 58 kda cyto keratin; keratin, type II cytoskeletal 5; cyto keratin 5</p> <p>keratin 5, type II, epidermal</p> <p>keratin 5</p> <p>keratin K5</p> <p>keratin 6A</p> <p>Similar to keratin 6A</p> <p>keratin 6a, type II</p> <p>Keratin, type II cytoskeletal 6A (Cytokeratin 6A) (CK 6A) (K6A keratin)</p> <p>keratin 6A; Keratin-6A; keratin, epidermal type II, K6A; cyto keratin 6A; 56 cyto skeletal type II keratin</p> <p>keratin 6B</p> <p>keratin 6B; keratin-6B; keratin, epidermal, type II, K6B; keratin, type II cyto skeletal 6B; cyto keratin 6B</p> <p>keratin 6C; keratin, epidermal type II, K6C; cyto keratin 6C; type II keratin isoform K6c</p> <p>Keratin, type II cytoskeletal 6C (Cytokeratin 6C) (CK 6C) (K6C keratin)</p> <p>keratin 6c, type II</p> <p>Keratin, type II cytoskeletal 6E (Cytokeratin 6E) (CK 6E) (K6E keratin)</p> <p>keratin 6 isoform K6e</p> <p>keratin 6f, type II</p> <p>Keratin, type II cytoskeletal 6F (Cytokeratin 6F) (CK 6F) (K6F keratin)</p>
NM_026352 NP_080628.1	U:(C-D)2.64	<p>cyclophilin</p> <p>cyclophilin-40</p> <p>peptidylprolyl isomerase CyP-40</p> <p>peptidylprolyl isomerase D (cyclophilin D); hCyP40</p> <p>peptidyl-prolyl isomerase G (cyclophilin G); Clk-associating RS-cyclophilin</p>

NM_009542	U:(IR-D)2.64	<p>40 kDa peptidyl-prolyl cis-trans isomerase (PPIase) (Rotamase) (Cyclophilin-40) (CYP-40) (Cyclophilin-related protein) CDC28/cdc2-like kinase associating arginine-serine cyclophilin CARS-Cyp SRcyp protein Zinc finger protein</p>
NP_033568.1		<p>Gonadotropin inducible transcription repressor Zinc finger protein 14 (Zinc finger protein KOX6) (Gonadotropin inducible transcription repressor-4) (GIOT-4) zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4 gonadotropin inducible transcription repressor-4 Similar to zinc finger protein 208 Kruppel-type zinc finger protein zinc finger protein 443; Kruppel-type zinc finger (C2H2) HSPC059 protein</p>
NM_020578	U:(C-IR)2.64	EH-domain
NP_065603.1		<p>EH-domain containing protein 1 (Testilin) (hPAST1) EH-domain containing 1; homolog of Drosophila past; EH domain containing 1; testilin EH domain containing protein 2 EH-domain containing protein 3 EH domain-containing protein-4 EH-domain containing 4; EH domain containing 4; ortholog of rat pincher EH-domain containing protein 4 (EH domain-containing protein FKSG7) (Hepatocellular carcinoma-associated protein 10/11) EH domain-containing protein FKSG7 Hpast hepatocellular carcinoma-associated protein HCA11 similar to Homo sapiens Hpast (HPAST) mRNA with GenBank Accession Number AF001434.1</p>
NM_007496	U:(C-D)2.63	binding protein
NP_031522.1		<p>alpha-fetoprotein enhancer-binding protein AT motif-binding factor 1 AT-binding transcription factor 1; AT motif-binding factor 1 Alpha-fetoprotein enhancer binding protein (AT motif-binding factor) (AT-binding transcription factor 1) zinc finger homeodomain protein</p>

NM_023118 NP_075607.1	U:(C-D)2.63 U:(C-IR)2.57	Zinc finger protein 409 phosphoprotein mitogen-responsive phosphoprotein disabled homolog 2; mitogen-responsive phosphoprotein disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein) Disabled homolog 2 (Differentially expressed protein 2) (DOC-2) DOC-2 disabled-2 disabled 2 p93 differentially expressed protein
NM_030127 NP_084403.1	U:(C-D)2.62	protease serine protease serin protease with IGF-binding motif HTRA serine protease HtrA-like serine protease Serine protease HTRA1 precursor (L56) serine protease Htra2 Serine protease HTRA2, mitochondrial precursor (High temperature requirement protein A2) (HtrA2) (Omi stress-regulated endoprotease) (Serine proteinase OMI) serine protease HtrA2-p7 serine protease HTRA3 Similar to serine protease HTRA3 Probable serine protease HTRA3 precursor Probable serine protease HTRA4 precursor protease, serine, 11 (IGF binding) protease, serine, 25 isoform 1 preproprotein; HtrA-like serine protease; high temperature requirement protein A2; Omi stress-regulated endoprotease novel serine protease, PRSS11
AK012045 BAB27991.1	U:(C-IR)2.61	kinase S6 kinase-related kinase S6 kinase b ribosomal protein S6 kinase 2 ribosomal protein S6 kinase 3 p70 S6 kinase Ribosomal protein S6 kinase (S6K) (p70-S6K)

<p>NM_011453</p> <p>NP_035583.1</p>	<p>U:(C-IR)2.61</p>	<p>p70 ribosomal S6 kinase alpha-I</p> <p>Ribosomal protein S6 kinase alpha 1 (S6K-alpha 1) (90 kDa ribosomal protein S6 kinase 1) (p90-RSK 1) (Ribosomal S6 kinase 1)(RSK-1) (pp90RSK1)</p> <p>p70 ribosomal S6 kinase alpha-II</p> <p>Ribosomal protein S6 kinase alpha 3 (S6K-alpha 3) (90 kDa ribosomal protein S6 kinase 3) (p90-RSK 3) (Ribosomal S6 kinase 2) (RSK-2) (pp90RSK2) (Insulin-stimulated protein kinase 1) (ISPK-1)</p> <p>p70 ribosomal S6 kinase beta</p> <p>Ribosomal protein S6 kinase beta 2 (S6K-beta 2) (70 kDa ribosomal protein S6 kinase 2) (p70-S6KB) (p70 ribosomal S6 kinase beta) (p70 S6Kbeta) (S6K2) (S6 kinase-related kinase) (SRK) (Serine/threonine-protein kinase 14 beta)</p> <p>ribosomal protein S6 kinase, 70kDa, polypeptide 1; ribosomal protein S6 kinase, 70kD, polypeptide 1; serine/threonine kinase 14 alpha</p> <p>ribosomal protein S6 kinase, 70kD, polypeptide 2</p> <p>ribosomal protein S6 kinase, 70kDa, polypeptide 2; ribosomal protein S6 kinase, 70kD, polypeptide 2; p70 ribosomal S6 kinase beta</p> <p>ribosomal protein S6 kinase, 90kD, polypeptide 1</p> <p>ribosomal protein S6 kinase, 90kDa, polypeptide 1; ribosomal protein S6 kinase, 90kD, polypeptide 1; Ribosomal protein S6 kinase, 90kD, 1</p> <p>ribosomal protein S6 kinase, 90kDa, polypeptide 3; ribosomal protein S6 kinase, 90kD, polypeptide 3</p> <p>ribosomal protein S6 kinase, long splice form</p> <p>serine/threonine kinase 14 beta</p> <p>insulin-stimulated protein kinase 1</p> <p>proteinase inhibitor</p> <p>serine (or cysteine) proteinase inhibitor</p> <p>serine proteinase inhibitor</p> <p>serine protease inhibitor 9</p> <p>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1</p> <p>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived</p> <p>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3</p> <p>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3; squamous cell carcinoma antigen 1</p> <p>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4; protease inhibitor (leucine-serpin); squamous cell carcinoma antigen 2; leupin</p> <p>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)</p> <p>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)</p> <p>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)</p> <p>proteinase inhibitor 8</p>
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		<p>proteinase inhibitor 9</p> <p>placental thrombin inhibitor</p> <p>Placental thrombin inhibitor (Cytoplasmic antiproteinase) (CAP) (Protease inhibitor 6) (PI-6)</p> <p>cytoplasmic antiproteinase; CAP</p> <p>cytoplasmic antiproteinase 2</p> <p>Cytoplasmic antiproteinase 2 (CAP2) (CAP-2) (Protease inhibitor 8) (Serin B8)</p> <p>cytoplasmic antiproteinase 3</p> <p>Cytoplasmic antiproteinase 3 (CAP3) (CAP-3) (Protease inhibitor 9)(Serin B9)</p> <p>thrombin inhibitor</p> <p>elastase inhibitor</p> <p>Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI)</p> <p>monocyte/neutrophil elastase inhibitor</p> <p>squamous cell carcinoma antigen</p> <p>squamous cell carcinoma antigen 1</p> <p>Squamous cell carcinoma antigen 1 (SCCA-1) (Protein T4-A)</p> <p>squamous cell carcinoma antigen 2</p> <p>Squamous cell carcinoma antigen 2 (SCCA-2) (Leupin)</p> <p>leupin</p> <p>leupin precursor</p>
<p>NM_007994</p> <p>NP_032020.1</p>	<p>U:(C-D)2.6</p> <p>U:(C-IR)2.58</p>	<p>phosphatase</p>
		<p>fructose-bisphosphatase</p> <p>fructose 1,6-bisphosphatase</p> <p>'fructose-1,6-bisphosphatase'</p> <p>fructose-1,6-bisphosphatase 2</p> <p>Fructose-1,6-bisphosphatase (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)</p> <p>fructose-1,6-bisphosphatase 1; fructose-bisphosphatase 1; liver</p> <p>fructose-bisphosphatase</p> <p>fructose-1,6-bisphosphatase 2; fructose-1,6-bisphosphatase isozyme 2; D-fructose-1,6-bisphosphate 1-phosphohydrolase; FBPase; muscle</p> <p>fructose-bisphosphatase; hexosediphosphatase</p> <p>Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)</p>
<p>NM_011498</p> <p>NP_035628.1</p>	<p>U:(C-D)2.6</p>	<p>transcription factor</p> <p>basic helix-loop-helix factor DEC1</p> <p>bHLH transcriptional factor DEC1</p>

		<p>bHLH transcription factor DEC1</p> <p>Class B basic helix-loop-helix protein 2 (bHLHB2) (Differentially expressed in chondrocytes protein 1) (DEC1) (Enhancer-of-split and hairy-related protein 2) (SHARP-2) (Stimulated with retinoic acid 13)</p> <p>basic helix-loop-helix protein, DEC2</p> <p>bHLH protein DEC2</p> <p>basic helix-loop-helix domain containing, class B, 3</p> <p>basic helix-loop-helix domain containing, class B, 3; bHLH protein DEC2</p> <p>Class B basic helix-loop-helix protein 3 (bHLHB3) (Differentially expressed in chondrocytes protein 2) (hDEC2) (Enhancer-of-split and hairy-related protein 1) (SHARP-1)</p> <p>differentiated embryo chondrocyte expressed gene 1</p>
NM_025749 NP_080025.1	U:(C-D)2.6	similar to RIKEN cDNA 4933409D10 [Mus musculus]
NM_027209 NP_081485.1	U:(C-D)2.6	<p>membrane-spanning 4-domains protein</p> <p>membrane-spanning 4-domains, subfamily A, member 6A</p> <p>MS4A6A protein</p> <p>MS4A6A-polymorph</p> <p>membrane-spanning 4-domains, subfamily A, member 6A isoform 2; CD20-like precursor; membrane-spanning 4-domains, subfamily A, member 6; four-span transmembrane protein 3.2; MS4A6A-polymorph; four-span transmembrane protein 3.1; HAIRB-iso</p> <p>membrane-spanning 4-domains, subfamily A, member 6A isoform 1; CD20-like precursor; membrane-spanning 4-domains, subfamily A, member 6; four-span transmembrane protein 3.2; MS4A6A-polymorph; four-span transmembrane protein 3.1; HAIRB-iso</p> <p>four-span transmembrane protein 3.1</p> <p>four-span transmembrane protein 3.2</p> <p>HAIRB-iso</p> <p>CDA01</p> <p>CD20-like precursor</p>
NM_026041 NP_080317.2	U:(C-D)2.6	CGI-115 protein
NM_008596 NP_032622.1	U:(C-D)2.6	<p>synaptoporin</p> <p>Similar to synaptorin</p> <p>synaptophysin</p> <p>synaptophysin; major synaptic vesicle protein P38</p>
NM_023684 NP_076173.1	U:(C-D)2.58	dJ583P15.4.1 (novel protein (translation of cDNA FLJ20406 (Em:AK000413)))
NM_007565 NP_031591.1	U:(C-D)2.57 U:(C-IR)2.66	ERF-2 protein

		<p>butyrate response factor 2; EGF-response factor 2; zinc finger protein, C3H type, 36-like 2</p> <p>Butyrate response factor 2 (TIS11D protein) (EGF-response factor 2) (ERF-2)</p> <p>Similar to butyrate response factor 2 (EGF-response factor 2)</p> <p>Tis11d</p>
NM_008986 NP_033012.1	U:(C-IR)2.57	<p>polymerase I and transcript release factor; RNA polymerase I and transcript release factor; TTF-I interacting peptide 12</p> <p>TTF-I interacting peptide 12</p>
NM_033398 NP_203971.1	U:(C-D)2.57	<p>leucine-zipper protein FKSG13</p> <p>receptor</p> <p>phosphatidylserine receptor</p> <p>PTDSR protein</p> <p>phosphatidylserine receptor; phosphatidylserine receptor beta</p> <p>phosphatidylserine receptor beta</p>
NM_008103 NP_032129.1	U:(C-IR)2.56	<p>transcription factor</p> <p>Glial cells missing protein</p> <p>GCM motif protein</p> <p>glide/gcm protein homolog</p> <p>glial cells missing protein homolog</p> <p>hGCMa</p> <p>glial cells missing homolog a; glial cells missing homolog 1</p> <p>chorion-specific transcription factor GCMa</p> <p>glial cells missing homolog 2; glial cells missing homolog b (Drosophila)</p>
NM_009914 NP_034044.1	U:(C-D)2.55	<p>receptor</p> <p>chemokine receptor</p> <p>chemokine (C-C motif) receptor 1; RANTES receptor</p> <p>C-C chemokine receptor type 1</p> <p>chemokine (C-C) receptor 1</p> <p>C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1) (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R) (RANTES-R) (HM145) (LD78 receptor)</p> <p>CC chemokine receptor 3</p> <p>chemokine (C-C motif) receptor 3</p> <p>similar to chemokine (C-C motif) receptor 3</p> <p>C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3)(CCR3) (Eosinophil eotaxin receptor)</p> <p>b-chemokine receptor CCR3</p> <p>CCR5 receptor</p>

NM_030714 NP_109639.1	U:(C-D)2.55	eosinophil eotaxin receptor macrophage inflammatory protein-1-alpha HM145 rhysin
AK020110 BAB31998.1	U:(C-D)2.55	rhysin 2 similar to rhysin 2 transcription factor
NM_013590 NP_038618.1	U:(C-D)2.55	hypothetical protein DKFZp566J091 likely ortholog of mouse limb-bud and heart gene lysozyme (renal amyloidosis)
NM_008718 NP_032744.1	U:(C-IR)2.55	lysozyme precursor Lysozyme C precursor (1,4-beta-N-acetylmuramidase C) lysozyme c precursor transcription factor
NM_019408 NP_062281.1	U:(C-D)2.54	single-minded (Drosophila) protein single-minded (Drosophila) homolog 1; Single-minded, drosophila, homolog of, 1 single-minded (Drosophila) homolog 2 short isoform; human transcription factor SIM2, homolog of the Drosophila single-minded gene SIM1 transcription factor SIM2 short form single-minded (Drosophila) homolog 2 long isoform; human transcription factor SIM2, homolog of the Drosophila single-minded gene SIM1 transcription factor SIM2 long form neutonal PAS domain protein basic-helix-loop-helix-PAS protein Neuronal PAS domain protein 1 (Neuronal PAS1) (Member of PAS protein 5) (MOP5) NPAS3 NPAS3 (MOP6) NPAS3 variant PAS protein 5 nuclear transcription factor NF-kB subunit transcription factor NF-kappa-B2, p49 splice form transcription factor NF-kappa-B2, p100 splice form Nuclear factor NF-kappa-B p100/p49 subunits (H2TF1) (Oncogene Lyt-10) (Lyt10) [Contains: Nuclear factor NF-kappa-B p52 subunit]

X80339 CAA56585.1	U:(C-IR)2.54	<p>nuclear factor of kappa light polypeptide gene enhancer in B-cells2 (p49/p100); Nuclear factor of kappa light chain gene enhancer in B-cells 2 Similar to nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100 p50-NF-kappa B homolog transcription factor NF-kappa-B2, p80 splice form p98=Rel/NF-kappa B p105 homolog [human, T lymphocytes, Peptide, 900 aa] transcription factor NF-kappa-B2, p105 splice form p80HT transcription factor</p> <p>homeobox transcription factor sine oculis homeobox protein sine oculis homeobox (Drosophila) homolog 1 Homeobox protein SIX1 (Sine oculis homeobox homolog 1) SIX1 SIX2 Homeobox protein SIX2 (Sine oculis homeobox homolog 2) sine oculis homeobox homolog 2 sine oculis homeobox homolog 2 (Drosophila) SIX3 protein sine oculis homeobox homolog 3 Homeobox protein SIX3 (Sine oculis homeobox homolog 3) SIX4 sine oculis homeobox homolog 4 Homeobox protein SIX4 (Sine oculis homeobox homolog 4) sine oculis homeobox homolog 6; optic homeobox 2; sine oculis homeobox (Drosophila) homolog 6; sine oculis homeobox homolog 6 (Drosophila) Homeobox protein SIX6 (Sine oculis homeobox homolog 6) (Optic homeobox 2) (Homeodomain protein OPTX2) homeodomain protein OPTX2 homeobox containing transcription factor SIX6 Six9 protein AREC3</p>
NM_009738 NP_033868.1	U:(C-D)2.53	<p>cholinesterase</p> <p>cholinesterase precursor Cholinesterase precursor (Acylcholine acylhydrolase) (Choline esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) butyrylcholinesterase butyrylcholinesterase precursor</p>

NM_011792
NP_035922.2

U:(C-D)2.53

acetylcholinesterase hydrophilic form precursor

Acetylcholinesterase precursor (AChE)

acetylcholinesterase precursor, brain splice form

acetylcholinesterase

acetylcholinesterase PI-linked form precursor

apoptosis-related acetylcholinesterase

neuroligin 2

similar to neuroligin 2 [Rattus norvegicus]

neuroligin 4; neuroligin X

neuroligin X

neuroligin Y

NLGN4 protein

Protease

type I integral membrane glycoprotein and aspartic protease

APP beta-secretase

beta-site APP cleaving enzyme

beta-site APP-cleaving enzyme 1 isoform A preproprotein; beta-site amyloid beta A4 precursor protein-cleaving enzyme; APP beta-secretase; aspartyl protease 2; beta-site amyloid precursor protein cleaving enzyme; memapsin-2; membrane-associated aspartic protease 2; transmembrane aspartic proteinase Asp2; beta-secretase

beta-site APP-cleaving enzyme 1 isoform B preproprotein; beta-site amyloid beta A4 precursor protein-cleaving enzyme; APP beta-secretase; aspartyl protease 2; beta-site amyloid precursor protein cleaving enzyme; memapsin-2; membrane-associated aspartic protease 2; transmembrane aspartic proteinase Asp2; beta-secretase

beta-site APP-cleaving enzyme 1 isoform C preproprotein; beta-site amyloid beta A4 precursor protein-cleaving enzyme; APP beta-secretase; aspartyl protease 2; beta-site amyloid precursor protein cleaving enzyme; memapsin-2; membrane-associated aspartic protease 2; transmembrane aspartic proteinase Asp2; beta-secretase

beta-site APP-cleaving enzyme 1 isoform D preproprotein; beta-site amyloid beta A4 precursor protein-cleaving enzyme; APP beta-secretase; aspartyl protease 2; beta-site amyloid precursor protein cleaving enzyme; memapsin-2; membrane-associated aspartic protease 2; transmembrane aspartic proteinase Asp2; beta-secretase

beta-site APP-cleaving enzyme 2 isoform A preproprotein; beta secretase 2; aspartyl protease 1; membrane-associate aspartic protease 1; memapsin-1; Down syndrome region aspartic protease; 56 kDa aspartic-like protease; beta-site amyloid beta A4 precursor protein-cleaving enzyme 2; transmembrane aspartic proteinase Asp1

Beta secretase 2 precursor (Beta-site APP-cleaving enzyme 2) (Aspartyl protease 1) (Asp 1) (ASP1) (Membrane-associated aspartic protease 1) (Memapsin-1)

NM_011603 NP_035733.1	U:(C-D)2.53	<p>Beta-secretase precursor (Beta-site APP cleaving enzyme) (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2) (Memapsin-2)</p> <p>beta-site APP cleaving enzyme I-432</p> <p>beta-site APP cleaving enzyme I-476</p> <p>beta-site APP cleaving enzyme I-457</p> <p>beta-site APP cleaving enzyme type C</p> <p>beta-site APP cleaving enzyme type B</p> <p>aspartyl protease</p> <p>aspartic-like protease</p> <p>aspartyl protease 1</p> <p>transmembrane aspartic proteinase Asp 1</p> <p>aspartyl protease 2</p> <p>transmembrane aspartic proteinase Asp 2</p> <p>aspartic proteinase BACE precursor</p> <p>memapsin 1</p> <p>memapsin 2</p> <p>transcription factor</p> <p>transcriptional activator</p> <p>TBP-like protein</p> <p>TBP-like 1</p> <p>TBP-like 1; TBP-like protein; TBP-related factor 2; TATA box binding protein-related factor 2; 21-kDa TBP-like protein; second TBP of unique DNA</p> <p>TATA box binding protein-like protein 1 (TBP-like protein 1) (TATA box binding protein-related factor 2) (TBP-related factor 2) (STUD protein) (21-kDa TBP-like protein)</p> <p>TATA box binding protein-related factor 2</p> <p>STUD protein</p>
NM_009748 NP_033878.1	U:(C-D)2.52	<p>transport protein</p> <p>BET</p> <p>BET1 homolog; Golgi vesicular membrane trafficking protein p18; Bet1p homolog, (hBET1)</p> <p>Bet1p homolog</p>
NM_011616 NP_035746.2	U:(C-D)2.52	<p>CD40 ligand</p> <p>CD40 surface protein</p> <p>CD40 antigen ligand; CD40 antigen ligand (hyper-IgM syndrome); T-B cell-activating molecule; TNF-related activation protein</p> <p>glycoprotein 39</p> <p>gp39=CD40 ligand [human, hyper-IgM syndrome patient JW, T cells, Peptide Partial Mutant, 151 aa]</p>

NM_008715 NP_032741	U:(C-IR)2.51	<p>Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (TNF-related activation protein) (TRAP) (T cell antigen Gp39) (CD154 antigen)</p> <p>helicase</p> <p>RNA helicase</p> <p>DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26</p> <p>DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26; RNA helicase HDB; deleted in cancer 1; RNA helicase HDB/DICE1; DEAD box protein similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26; deleted in cancer 1; RNA helicase HDB/DICE1; DEAD box protein; RNA helicase HDB candidate tumor suppressor protein DICE1</p> <p>RNA helicase HDB/DICE1</p> <p>NOTCH 2</p> <p>notch 2 preproprotein</p> <p>Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hN2)</p> <p>Notch homolog 2 (Drosophila)</p>
NM_011086 NP_035216.1	U:(C-D)2.5	<p>kinase</p> <p>FYVE finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate 5-kinase) (PIP5K) (PtdIns(4)P-5-kinase) (p235)</p> <p>similar to FYVE finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) (p235)</p> <p>similar to FYVE finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate 5-kinase) (PIP5K) (PtdIns(4)P-5-kinase) (p235)</p>
NM_013820 NP_038848.1	U:(C-D)1.77	<p>kinase</p> <p>hexokinase</p> <p>hexokinase I</p> <p>hexokinase 1 isoform ta/tb</p> <p>hexokinase 1 isoform HKI-ta/tb; brain form hexokinase</p> <p>hexokinase 1 isoform td</p> <p>hexokinase 1 isoform HKI-td; brain form hexokinase</p> <p>hexokinase 1 isoform HKI; brain form hexokinase</p> <p>hexokinase II</p> <p>hexokinase 2; hexokinase-2, muscle</p> <p>Hexokinase, type II (HK II) (Muscle form hexokinase)</p> <p>Human hexokinase II cDNA</p>
NM_007381 NP_031407.1	U:(C-D)1.74	<p>dehydrogenase</p> <p>acyl-CoA dehydrogenase</p>

NM_026268
NP_080544.1

U:(C-D)1.66

short chain acyl CoA dehydrogenase
 short chain acyl-CoA dehydrogenase precursor
 acyl-CoA dehydrogenase precursor, short-chain-specific
 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
 acyl-CoA dehydrogenase short/branched chain specific precursor
 Acyl-CoA dehydrogenase, short/branched chain specific, mitochondrial
 precursor (SBCAD) (2-methyl branched chain acyl-CoA dehydrogenase)
 (2-MEBCAD) (2-methylbutyryl-coenzyme A dehydrogenase)
 (2-methylbutyryl-CoA dehydrogenase)
 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain precursor
 Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor
 (SCAD) (Butyryl-CoA dehydrogenase)
 acyl-Coenzyme A dehydrogenase, long chain precursor
 long chain acyl-CoA dehydrogenase
 long-chain-acyl-CoA dehydrogenase precursor, mitochondrial
 Acyl-CoA dehydrogenase, long-chain specific, mitochondrial precursor
 (LCAD)
 Similar to acyl-Coenzyme A dehydrogenase, long chain
 isovaleryl dehydrogenase
 isovaleryl-coA dehydrogenase (IVD)
 isovaleryl Coenzyme A dehydrogenase
 Isovaleryl-CoA dehydrogenase, mitochondrial precursor (IVD)
 isovaleryl-CoA dehydrogenase precursor
 phosphatase
 negatively regulates MAP kinases and ERK2
 protein-tyrosine-phosphatase
 dual specificity phosphatase 6
 DUSP6
 Dual specificity protein phosphatase 6 (Mitogen-activated protein kinase
 phosphatase 3) (MAP kinase phosphatase 3) (MKP-3) (Dual specificity protein
 phosphatase PYST1)
 dual specificity phosphatase 6 isoform a; MAP kinase phosphatase 3;
 serine/threonine specific protein phosphatase
 dual-specificity phosphatase 7 PYST2-L
 Dual specificity protein phosphatase 7 (Dual specificity protein phosphatase
 PYST2)
 similar to dual-specificity phosphatase 7 PYST2-L
 dual specificity phosphatase 9; map kinase phosphatase 4; serine/threonine
 specific protein phosphatase
 Dual specificity protein phosphatase 9 (Mitogen activated protein kinase
 phosphatase 4) (MAP kinase phosphatase 4) (MKP-4)
 Similar to dual specificity phosphatase 9

NM_028780 NP_083056.2	U:(C-D)1.65	<p>mitogen-activated protein kinase phosphatase 4</p> <p>multispanning membrane protein</p> <p>transmembrane 9 superfamily member 1; multispanning membrane protein (70kD); transmembrane protein 9 superfamily member 1</p> <p>Transmembrane 9 superfamily protein member 1 precursor (hMP70)</p> <p>transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2</p> <p>Transmembrane 9 superfamily protein member 2 precursor (p76)</p> <p>Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-iso)</p> <p>transmembrane protein TM9SF3</p> <p>Transmembrane 9 superfamily protein member 4</p> <p>endomembrane protein emp70 precursor isolog</p> <p>Similar to <i>S.cerevisiae</i> EMP70 protein precursor (S25110)</p> <p>SM-11044 binding protein</p>
NM_007912 NP_031938.1	U:(C-IR)1.67	<p>receptor</p> <p>growth factor receptor</p> <p>epidermal growth factor receptor</p> <p>truncated epidermal growth factor receptor</p> <p>aberrant epidermal growth factor receptor</p> <p>epidermal growth factor receptor, HER4</p> <p>epidermal growth factor receptor precursor</p> <p>Epidermal growth factor receptor precursor (Receptor protein-tyrosine kinase ErbB-1)</p> <p>truncated epidermal growth factor receptor precursor</p> <p>truncated epidermal growth factor receptor-like protein precursor</p> <p>p60 epidermal growth factor receptor</p> <p>p110 epidermal growth factor receptor</p> <p>A431-specific p115 epidermal growth factor receptor</p> <p>p170 epidermal growth factor receptor</p> <p>Receptor protein-tyrosine kinase erbB-4 precursor (p180erbB4) (Tyrosine kinase-type cell surface receptor HER4)</p> <p>EGF (1 is 2nd base in codon)</p> <p>receptor tyrosine kinase</p> <p>v-erb-a erythroblastic leukemia viral oncogene homolog 4; avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 4; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4</p>
NM_020614 NP_065639.1	U:(C-IR)1.56	<p>transcription factor</p> <p>TBP-associated factor 1B; TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kD; SL1, 63kD subunit</p>

		transcription factor SL1
AK016618 BAB30341.1	U:(C-D)+2.0	PF20; sperm-associated WD repeat protein
	U:(C-IR)+1.9	
AK016718 XP_111038	U:(C-D)+2.2	tektin 3
	U:(C-IR)+1.9	tektin 1
		tektin 3; testicular microtubules-related protein
NM_008919 2207219A	U:(C-D)+1.9	neuropeptide y receptor
	U:(C-IR)+1.9	
		pancreatic polypeptide receptor
		pancreatic polypeptide receptor 1
		neuropeptide Y receptor Y1; Neuropeptide Y receptor
NM_018789 Q9WVH3	U:(C-D)+1.8	fork head protein
	U:(C-IR)+1.8	
		forkhead box O1A
		forkhead box O3A;
		orkhead transcription factor AFX variant zeta
		Forkhead box protein O4
NM_021371 NP_067346.1	U:(C-D)+2.3	calneuron 1; calcium-binding protein CABP8
	U:(C-IR)+1.9	

Subtable 2C: Mixed Mouse Genes/Proteins and Human Protein Classes

Accession Number	Accession Number	Accession Number
NM_009020	U:(C-D)2.52	
NP_033046.1	F:(IR-D)+4.59	RAG2 HUMAN V(D)J recombination activating protein 2 (RAG-2)
		recombination activating gene 2
		recombination activating protein 2
		RAG2

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susceptibility. Diabetes 52:688-700.

Citation of documents herein is not intended as an admission that any of the documents cited herein is pertinent prior art, or an admission that the cited documents is considered material to the patentability of any of the claims of the present application. All statements as to the date or representation as to the contents of these documents is based on the information available to the applicant and does not constitute any admission as to the correctness of the dates or contents of these documents.

The appended claims are to be treated as a non-limiting recitation of preferred embodiments.

In addition to those set forth elsewhere, the following references are hereby incorporated by reference, in their most recent editions as of the time of filing of this application: Kay, Phage Display of Peptides and Proteins: A Laboratory Manual; the John Wiley and Sons Current Protocols series, including Ausubel, Current Protocols in Molecular Biology; Coligan, Current Protocols in Protein Science; Coligan, Current Protocols in Immunology; Current Protocols in Human Genetics; Current Protocols in Cytometry; Current Protocols in Pharmacology; Current Protocols in Neuroscience; Current Protocols in Cell Biology; Current Protocols in Toxicology; Current Protocols in Field Analytical Chemistry; Current Protocols in Nucleic Acid Chemistry; and Current Protocols in Human Genetics; and the following Cold Spring Harbor Laboratory publications: Sambrook, Molecular Cloning: A Laboratory Manual; Harlow, Antibodies: A Laboratory Manual; Manipulating the Mouse Embryo: A Laboratory Manual; Methods in Yeast Genetics: A Cold Spring Harbor Laboratory Course Manual; Drosophila Protocols; Imaging Neurons: A Laboratory Manual; Early Development of *Xenopus laevis*: A Laboratory Manual; Using Antibodies: A Laboratory Manual; At the Bench: A Laboratory Navigator; Cells: A Laboratory Manual; Methods in Yeast Genetics: A Laboratory Course Manual; Discovering Neurons: The Experimental Basis of Neuroscience; Genome Analysis: A Laboratory Manual Series; Laboratory DNA Science; Strategies for Protein Purification and Characterization: A Laboratory Course Manual; Genetic Analysis of Pathogenic

Bacteria: A Laboratory Manual; PCR Primer: A Laboratory Manual; Methods in Plant Molecular Biology: A Laboratory Course Manual; Manipulating the Mouse Embryo: A Laboratory Manual; Molecular Probes of the Nervous System; Experiments with Fission Yeast: A Laboratory Course Manual; A Short Course in Bacterial Genetics: A Laboratory Manual and Handbook for Escherichia coli and Related Bacteria; DNA Science: A First Course in Recombinant DNA Technology; Methods in Yeast Genetics: A Laboratory Course Manual; Molecular Biology of Plants: A Laboratory Course Manual.

All references cited herein, including journal articles or abstracts, published, corresponding, prior or otherwise related U.S. or foreign patent applications, issued U.S. or foreign patents, or any other references, are entirely incorporated by reference herein, including all data, tables, figures, and text presented in the cited references. Additionally, the entire contents of the references cited within the references cited herein are also entirely incorporated by reference.

Reference to known method steps, conventional methods steps, known methods or conventional methods is not in any way an admission that any aspect, description or embodiment of the present invention is disclosed, taught or suggested in the relevant art.

The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art (including the contents of the references cited herein), readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the

teachings and guidance presented herein, in combination with the knowledge of one of ordinary skill in the art.

Any description of a class or range as being useful or preferred in the practice of the invention shall be deemed a description of any subclass (e.g., a disclosed class with one or more disclosed members omitted) or subrange contained therein, as well as a separate description of each individual member or value in said class or range.

The description of preferred embodiments individually shall be deemed a description of any possible combination of such preferred embodiments, except for combinations which are impossible (e.g, mutually exclusive choices for an element of the invention) or which are expressly excluded by this specification.

If an embodiment of this invention is disclosed in the prior art, the description of the invention shall be deemed to include the invention as herein disclosed with such embodiment excised.

CLAIMS

1. A method of protecting a human subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state, which comprises administering to the subject a protective amount of an agent which is

(1) a polypeptide which is substantially structurally identical or conservatively identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1A and 1C, or (b) selected from the group consisting of human proteins within at least one of the human protein classes set forth in master table 2, subtables 2A and 2C,

or

(2) an expression vector encoding the polypeptide of (1) above and expressible in a human cell, under conditions conducive to expression of the polypeptide of (1);

where said agent protects said subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state.

2. A method of protecting a human subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state which comprises administering to the subject a protective amount of an agent which is

(1) an antagonist of a polypeptide, occurring in said subject, which is substantially structurally identical or conservatively identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtable 1B and 1C, or (b) selected from the group consisting of human

proteins belonging to at least one of the human protein classes set forth in master table 2, subtables 2B and 2C,

(2) an anti-sense vector which inhibits expression of said polypeptide in said subject,

where said agent protects said subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state.

3. A method of screening for human subjects who are prone to progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state, which comprises assaying tissue or body fluid samples from said subjects to determine the level of expression of a "favorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or conservatively identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1A and 1C, or (b) selected from the group consisting of human proteins within at least one of the human protein classes set forth in master table 2, subtables 2A and 2C,

and directly correlating the level of expression of said marker gene with the propensity to progression in said patient.

4. A method of screening for human subjects who have a propensity for progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state, which comprises assaying tissue or body fluid samples from said subjects to determine the level of expression of an "unfavorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or conservatively identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human

proteins set forth in master table 1, subtable 1B and 1C, or (b) selected from the group consisting of human proteins belonging to at least one of the human protein classes set forth in master table 2, subtables 2B and 2C;

5

and inversely correlating the level of expression of said marker gene with the propensity to progression in said patient.

10

5. The method of claims 1 or 3 in which the reference protein is of subtable 1A or of a class set forth in subtable 2A.

15

6. The method of claims 1 or 3 in which the reference protein is of subtable 1B or of a class set forth in subtable 2B.

7. The method of any one of claims 1-6 in which (a) applies.

20

8. The method of any one of claims 1-7 in which the reference protein is a human protein.

25

9. The method of any one of claims 1-7 in which the reference protein is a mouse protein.

10. The method of any one of claims 3 or 4 in which the level of expression of the marker protein is ascertained by measuring the level of the corresponding messenger RNA.

30

11. The method of any one of claims 3 or 4 in which the level of expression is ascertained by measuring the level of a protein encoded by said marker gene.

35

12. The method of any one of claims 1-9 in which said polypeptide is at least 80% identical or at least highly conservatively identical to said reference protein.

13. The method of any one of claims 1-10 in which said polypeptide is at least 90% identical to said reference protein.

14. The method of any one of claims 1-11 in which said polypeptide is identical to said reference protein.

5 15. The method of any one of claims 1-14 in which the E-value cited for the reference protein in Master Table 1 is not more than e-6.

10 16. The method of claim 15 in which the E-value cited for the reference protein in Master Table 1 is less than e-10.

15 17. The method of claim 17 in which the E value calculated by BLASTN or BLASTX would be less than e-15, more preferably less than e-20, still more preferably less than e-40, even more preferably less than e-60, considerably more preferably less than e-80, and most preferably less than e-100.

20 18. The method of any of claims 2-17 in which the antagonist is an antibody, or an antigen-specific binding fragment of an antibody.

19. The method of any of claims 2-17 in which the antagonist is a peptide, peptoid, nucleic acid, or peptide nucleic acid oligomer.

25 20. The method of any of claims 2-17 in which the antagonist is an organic molecule with a molecular weight of less than 500 daltons.

30 21. The method of claim 20 in which said organic molecule is identifiable as a molecule which binds said polypeptide by screening a combinatorial library.

Figure 1(a)

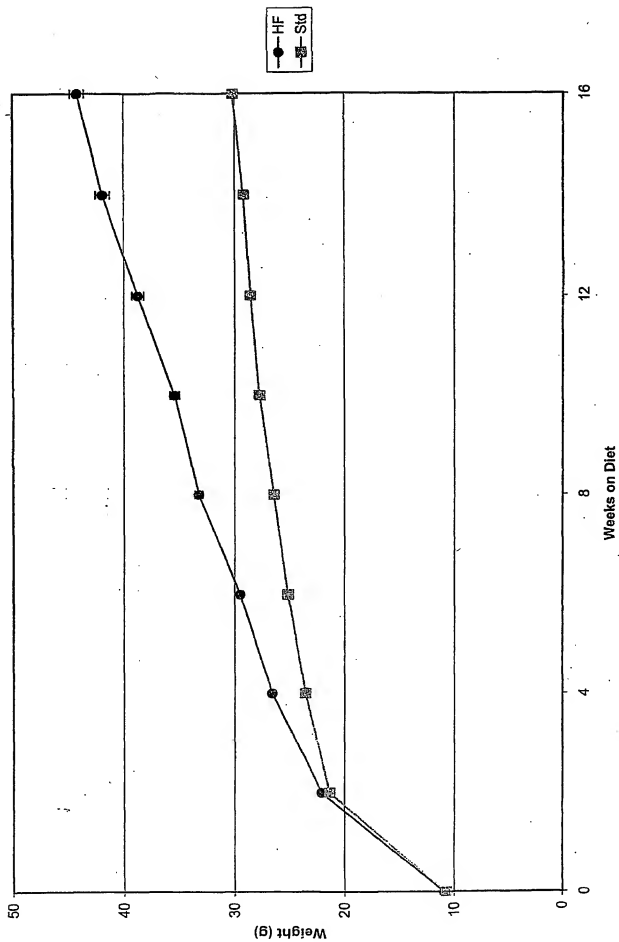


Figure 1(b)

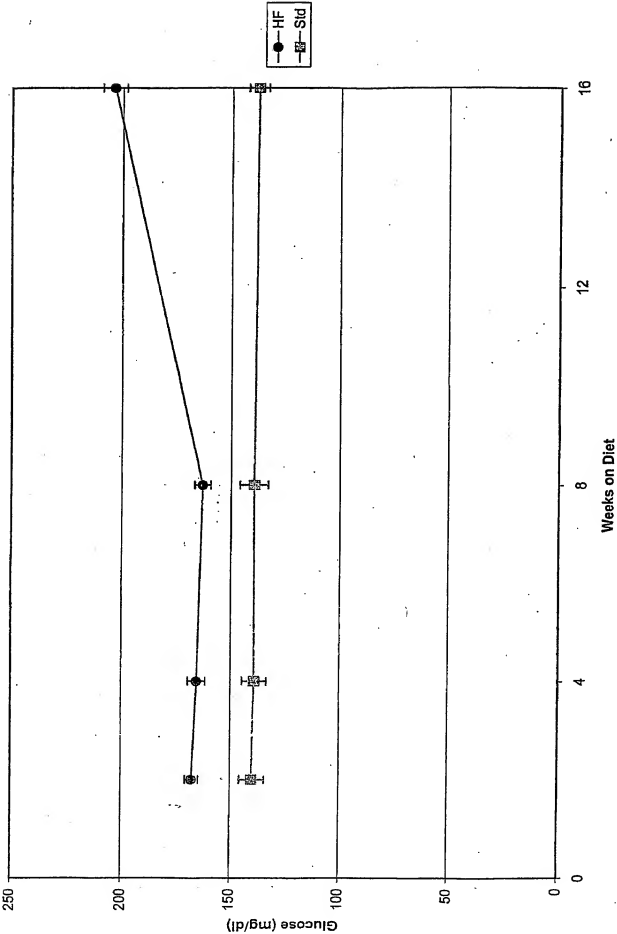


Figure 1(c)

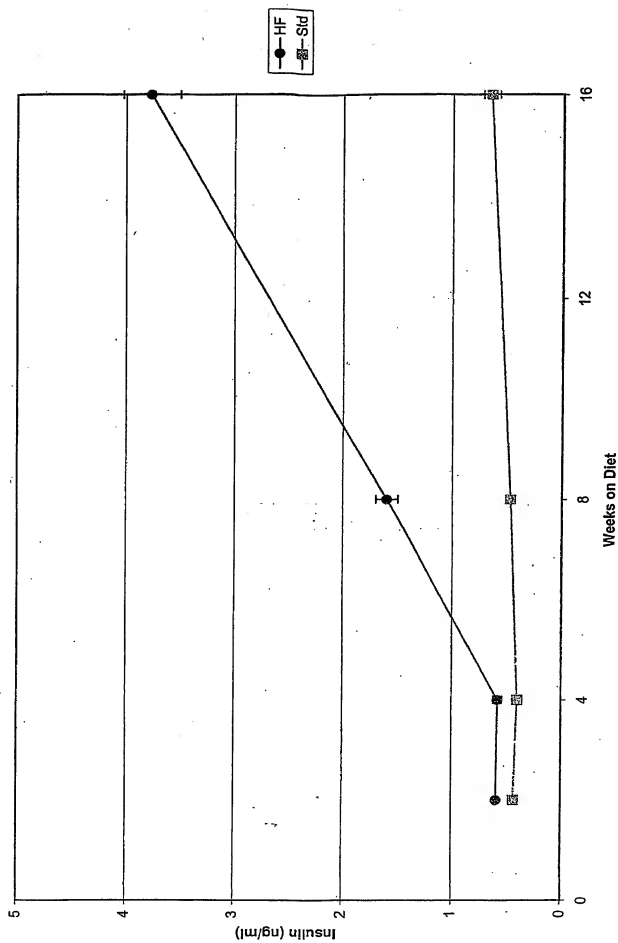


Figure 2

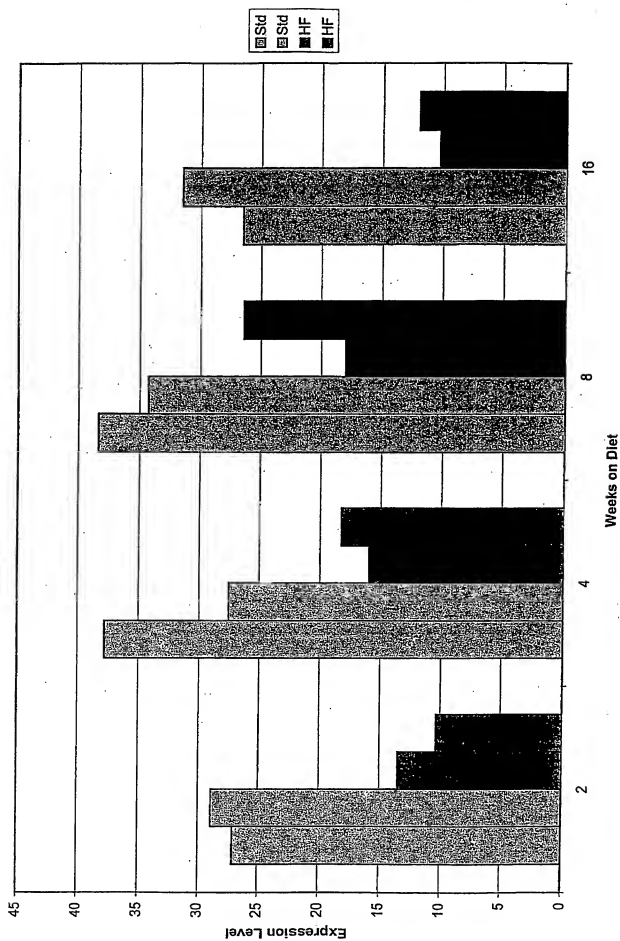
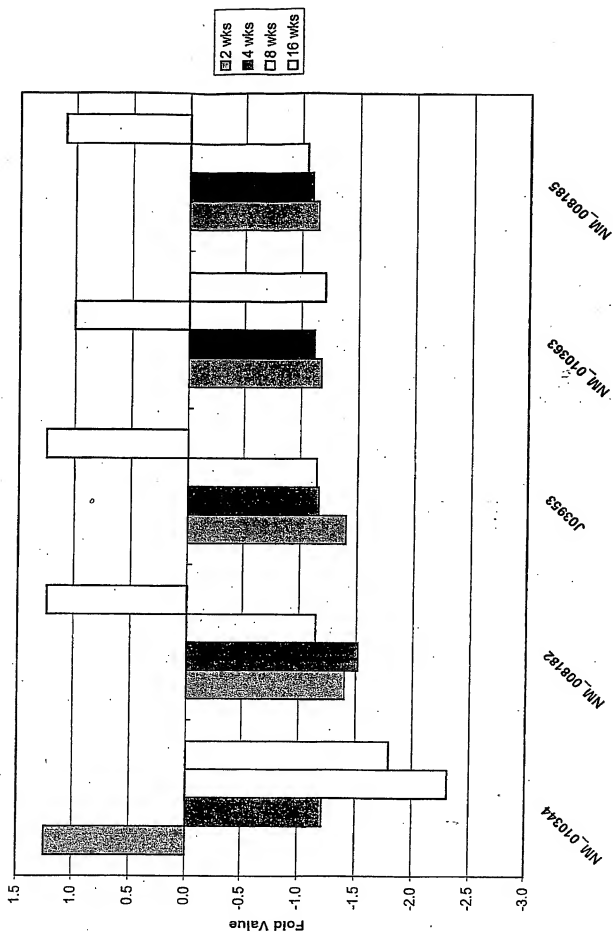


Figure 3



INTERNATIONAL SEARCH REPORT

International Application No.

...T/US2004/036760

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 A61K38/53 C12Q1/68 G01N33/50 A61P3/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 A61K C12Q G01N A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, Sequence Search, BIOSIS, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	LIM, H.W. ET AL.: "Identification of differentially expressed mRNA during pancreas regeneration of rat by mRNA differential display" BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 299, no. 5, 20 December 2002 (2002-12-20), pages 806-812, XP002324520 cited in the application the whole document see especially: page 807, column 1, line 4 - line 15 page 809; tables 2,3 page 811, column 1, line 47 - column 2, line 15 ----- -/-	1-18
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

14 April 2005

Date of mailing of the international search report

27/04/2005

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Authorized officer

Fuchs, U

INTERNATIONAL SEARCH REPORT

International Application No

US2004/036760

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>BERNAL-MIZRACHI, E. ET AL.: "Gene expression profiling in islet biology and diabetes research" DIABETES/METABOLISM RESEARCH AND REVIEWS, vol. 19, no. 1, February 2003 (2003-02), pages 32-42, XP008045358 cited in the application the whole document see especially: page 38, column 1, line 10 - page 41, column 1, line 48</p>	1-18
A	<p>WINZELL, M.S. ET AL.: "Downregulation of islet hormone-sensitive lipase during long-term high-fat feeding" BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 304, no. 2, 2 May 2003 (2003-05-02), pages 273-278, XP002324521 the whole document see especially: page 276; figure 5</p>	1-18
A	<p>COROMINOLA, H. ET AL.: "Identification of Novel Genes Differentially Expressed in Omental Fat of Obese Subjects and Obese Type 2 Diabetic Patients" DIABETES, vol. 50, no. 12, December 2001 (2001-12), pages 2822-2830, XP002293068 the whole document see especially: page 2827; table 4</p>	1-18
A	<p>ROBERTSON, R.P. ET AL.: "Glucose Toxicity in beta-Cells: Type 2 Diabetes, Good Radicals Gone Bad, and the Glutathione Connection" DIABETES, vol. 52, no. 3, March 2003 (2003-03), pages 581-587, XP002324519 the whole document see especially: page 584, column 2, line 2 - page 585, column 2, line 17; figure 4; table 1</p>	1-18
A	<p>WO 99/06059 A (BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM; BETAGENE, INC.) 11 February 1999 (1999-02-11) the whole document</p>	1-18

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2004/036760

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 1, 2, 5-9, 12-18 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.: 19-21
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box II.1

Although claims 1, 2, 5-9, 12-18 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box II.2

Claims Nos.: 19-21

Present claims 19-21 relate to a compound defined by reference to a desirable characteristic or property, namely being "an antagonist of a polypeptide ... which is substantially structurally identical or conservatively identical in sequence to a reference protein which is a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtable 1B or 1C, or b) selected from the group consisting of human proteins belonging to at least one of the human protein classes set forth in master table 2, subtables 2B and 2C".

The claims cover all compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search impossible. Consequently, no search has been carried out for claims 19-21.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

/US2004/036760

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9906059	A	11-02-1999	AU 8671798 A	22-02-1999
			WO 9906059 A2	11-02-1999
			US 6171856 B1	09-01-2001
<hr/>				